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e e	HUMALCE221	-	HSLDLRN2				HUMALCE221	HSU67804	Ξ				_			HUMHGAL	HUMLDLRF		G32614	Ξ	_				×	HS8IC8R	HUMALCE272	HUMALCE16		•	HUMLDLRA2	HUMLDLRA1	HUMLDLRA2	HUMLDLRDJ			G43538	HUMALCE43	Ξ				HSSTHPKIB	NVIHIS2A
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ALIGNMENTS

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1 (bases 1 to 107)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
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1 (bases 1 to 103)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
              HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Homo sapiens
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30 c 35 q 1
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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1 (bases 1 to 108)

Horsthemke, B., Belselgel, U., Dunning, A., Havinga, J.R.,
Milliamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
BNT 5. Biochem. 164 (1), 77-81 (1987)
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1 (bases 1 to 108)

1 (bases 1 to 108)

Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. 3. Blochem. 164 (1), 77-81 (1987)
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HSLDLRN2 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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Human LDL-receptor gene intron 14 fragment (normal gene)
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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                                                                              3624 TCACTGCAAGCTCTGCCTCCCGGGTTTATGCCATTCTCATGTC 3666
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1.108
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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                                                                                                                                                                                                                                                                                            3 AAAAATTAGCCAGGCGTGGCAGGTGCCAGCTGTAATCCCAGCTACTCGGAGGCTGAGGC 62
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 0.00021;
0; Mismatches 17;
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Pred. No. 4.5e-05;
0; Mismatches 14
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .108
/note="intron XIV fragment"
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Best Local Similarity 84.1%;
Matches 90; Conservative
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Best Local Similarity 86.83
Matches 92; Conservative
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See X05250 for corresponding normal gene sequence In the defective LDL-receptor gene the deletion ocurred between two allu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
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Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
                           Human LDL-receptor mutated gene with intron 14 deletion junction.
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1 (bases I to 108)
Shaikh, T. H.. Roy, A. M., Kim, J., Batzer, M. A. and Deininger, P. L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                 Homo saplens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
20-MAY-1992
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                                                                                                                 Alu repetitive sequence; low density lipoprotein receptor
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
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Human small cytoplasmic Alu transcript.
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108 bp
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U67803.1 GI:2289917
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U67804.1 GI:2289918
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Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
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1 (bases 1 to 103)

2 Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcripts in human embryonal carcinoma cells. J. Mol. Blol. (1992) In press
J. Mol. Blol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          97 GTAGAGACGGGGTTTCACCTTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 38
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
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Homo sapiens
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Pred. No. 0.00019;
0; Mismatches 10;
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Human small cytoplasmic Alu transcript.
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                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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27 c 33 g 1
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/rpt_type=dispersed
39 c 30 g
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/note="scAlu"
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Matches 86; Conservative
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Direct Submission
Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo
Matoba, Osaka University, Institute for Molecular and Cellular Blo;
H-3, Yamada-cka, Suita, Osaka 565, Japan
(E-mail:matoba@inherit.imcb.osaka-u.ac.jp,
Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
2 (bases 1 to 108)
Matoba, R., Okubo, K., Hori, N., Fukushima, A. and Matsubara, K.
The addition of 5'-coding information to a 3'-directed cDNA library improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
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J. Mol. Biol. 271 (2), 222-234 (1997)
97415756
2 (bases 1 to 108)
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene signature.
Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
Homo sapiens
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Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 108)
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
                                                                                     Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Best Local Similarity 86.5%; Pred. No. 0.0013;
Matches 83; Conservative 0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
/rpt_type=dispersed
38 c 26 g
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note="scAlu"
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12264 GTAGCTGGGATTACAGGCATGCGCCACGACACCTGGCTAATTT 12307
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                                                                                  RESULT 12
HSU67807/c
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MEDLINE
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LOCUS
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1 (bases 1 to 108)

Horsthemke, B., Basislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
Bur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
                                                                                                                                                                                                                                                                                                                                                      12200 GATCTTGGCTCACAGCAACCTCCGGCTTCCAAGCCATTCTCTGCTTAGGCCTC 12259
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                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                          108 GATCTTGGCTCACTGCAACCTGCTGCCTCCCGGGNTCAAGCGACTCTCCTGCCTCAGCCTC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TCGCCTCACCACAACCTCTGCCTCCTGGGTTCAAACCATTTTCCTGCCTCAGCCTCTA 61
Research Institute of Innovative Technology for the Earth 9-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alu repetitive sequence; low density lipoprotein receptor; repetitive sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Qy 12260 CGGAGTAGCTGGGATTACAGGCATGCGCCACGACACCCTGGCTAATTTT 12308
                                                                                                                                                                                                                                                                                      Length 108;
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                                                                                                                                                                                    Score 74.2; DB 9; I
Pred. No. 0.0019;
); Mismatches 15;
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38 c 20 g 29 t
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/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
                                                                                                                                 /organism="Homo saplens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                       38 g
                                                                                                                                                                                                                                                                                      0.3%;
                 Kizugawadai Kizu-cyo,
Soraku-gun, Kyoto
                                                                                                                                                                                                     /sex-"Male"
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                                                Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321
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Best Local Similarity 85.3%
Matches 93; Conservative
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Best Local Similarity
Matches 85; Conserv
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HSLDLI12
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-AdG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 110)
Shaikh, T. H., Roy, A., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAS derived from primary and small cytoplasmic Alu (scAlu)
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 103)
                                                                                                                                                 01-AUG-1997
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Direct Submission
Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler, R., Riley, J.H., Ogilvie, D.J., Anand, R., Buxton, J.,
Davies, J., Johnson, K. and Markham, A.F.
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Human sequence tagged site BICBR DNA from 19q13.
X57789
62 GTAGCTGGGATTACAAGCATGTGCCACCACCACCGGCTGATTT 105
                                                                                                                                                    PRI
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Human small cytoplasmic Alu transcript.
U67807
U67807.1 GI:2289921
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu6"
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/rpt_type=dispersed
39 c 24 g
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STS; myotonic dystrophy.
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Best Local Similarity 83.8<sup>3</sup>
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcripts
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BASE COUNT
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                                                                                                                                           RESULT 15
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COMMENT
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                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. Walliamson, R. and Humphries, S. Onequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia BTI or J. Blochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1...108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSLDLRD1 108 bp DNA PRI 20-MAY-1992 Human LDL-receptor mutated gene with intron 12 deletion junction.
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                                                                                                                                                                                                                                                                                                                                                                                                                          6395 ATTAGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGA 6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="deletion junction region intron 12/ intron 15" 40~{
m c} 20 g t
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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                                                                                                                                                                                                                                                                  1 others
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Pred. No. 0.0031;
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Nucleic Acids Res. 19 (17), 4787 (1991)
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/clone_lib="YAC library: ICI"
/clone="8IC8"
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                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                               See also X57788 for STS 8IC8L.
                                                                                                  Location/Qualifiers
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83.78;
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Matches 85; Conservative
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Source: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
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1 (bases 1 to 108)

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Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia for Eur.

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7 Elochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
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106 AAAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
                                                                                                                                                                                                                                                                                                                                                                                              Alu repetitive sequence; low density lipoprotein receptor
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Copyright (c) 1993 - 2000 Compugen Ltd
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Claim 1: Page 218; 310pp; English.

X10269-X1237 are human DNA fragments which contain biallelic polymorphic
X10269-X1237 are human DNA fragments which contain biallelic polymorphic
X10269-X1237 are human DNA fragments which have been isolated using the primers represented in
X09121-X10268. The base occupying the polymorphic site is indicated by
the appropriate IUPAC-IUB ambiguity code. These fragments can be used in
methods for determining polymorphic forms in an individual for use in
e.g. forensics, paternity testing or for phenotypic typing for diseases
such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
muscular dystrophy, Wiskott-Aldrich syndrome, Pabry & disease, familial
hypercholesterolemia, polycystic kidney disease, hereditary
spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
contribute telangiectesia, familial colonic polyposis, Ehlers-Danlos
syndrome, osteogenesis imperfecta, acute intermittent porphyria,
autoimmune diseases, inflammation, cancer, diseases of the nervous
syndrome, osteogenesis imperfecta microrganisms, and characteristics such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMAR-1999 (first entry)

Human biallelic polymorphic DNA fragment EST98276b.

Polymorphism, biallelic, human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
treatment; marker; ss.
                                                                                    Human biallelic polymorphic DNA fragment EST98276c.
Polymorphism, biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED) WHITEHEAD INST BIOMEDICAL RES.
HUGSON T. Lander ES. Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity
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Pred. No. 0.058;
1; Mismatches 20; Indels (
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                               X12085 standard; DNA; 100 BP.
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Sequence 100 BP; 22 A;
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06-NOV-1996; US-030455.
                                                                                                                                                                   treatment; marker; ss
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Pure No. 1. Lander L. 2. Many 2., New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease

PT determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease

CI aim 1; Page 219; 310pp; English.

CI X10280-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in comparisons. The page 219; 310pp; English.

CI X10280-X12937 are human DNA fragments which contain biallelic polymorphic comparisons. The appropriate IUPAC-IUB ambiguity code. These fragments can be used in comparison for determining polymorphic forms in an individual for use in comparisons, page and the sample of the code of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22975 GTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCTGAAGAAGGAGGATCGCTTGAGTC 23034
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Sequences shown in V41230 to V41247 represent nucleotide sequences of Sequences shown in V41230 to V41247 represent nucleotide sequences of mouse EST from tagged CDNA clones. These are used in the method of the invention of screening for human developmental genes. The method comprises inserting a promoterless reporter gene into a non-primate mammalian embryonic stem cell (ESC) genome and identifying cellular transcripts that encode the reporter gene product. Fragments of genes encoding these transcripts are cloned and sequenced. A gene encoding a transcript that includes unknown sequences is selected and expression level of the gene encoding the transcript, or part of it, in different cell types and/or different developmental stages is detected. A gene showing differential expression is selected and expression levels of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 GTGACTCACACCTATAATCCTGGCACTTTAGGAGGCTKAGGAAGGAGGGGGTTGTTGAAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryonic stem cells and analysing differential expression in vitro, selecting homologous non-human primate gene and using it to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for human developmental genes - by trapping in murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66.6; DB 1; Length 100;
Pred. No. 0.058;
1; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse embryonic cell EST 13-4 nucleotide sequence.
Embryonic stem cell; ESC; non-primate; mouse; EST; human;
developmental gene; transgenic animal; reporter gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 23035 CGGGAGTTCAAGAGCATCCTGGGCAACACAGGGAGACCC 23073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 CAGGAGCTCAAGACCATCCTGGGAAACATAGCAAGACTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 66.6; 78.8%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1996; US-032510.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such diseases.
BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V41231 standard; cDNA; 86 BP
Hudson T, Lander ES, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V41231;
01-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 78.8
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORR ) CORNELL RES FC
Holzschu DL, Mark WH;
WPI; 98-322656/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1998.
25-NOV-1997; U22335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09823633-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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determining polymorphic forms for use in e.g. forensics, paternity

PT determining polymorphic forms for disease

Calain 1: Page 219: 310pp: English.

Cx10269-X12937 are human DNA fragments which contain biallelic polymorphic

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

Cx10269-X120368 The base occupying the polymorphic site is indicated by

Cx 09121-X10268 The base occupying the polymorphic site is indicated by

Cx 09121-X10268 The base occupying the polymorphic site is indicated by

Cx 09121-X10268 The base occupying the polymorphic such can be used in

Cx 09121-X10268 The base occupying the polymorphic such occupancy in the second of the superpriate IUPAC-IUB ambiguity ocder. These fragments can be used in

Cx methods for determining polymorphic forms in an individual for use in

Cx of cremsics, paternity testing or for phenotypic typing for diseases

Cx or forensics, paternity alaberes insipidus, Lesch-Nyhan syndrome,

Cx muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial

Cx oppercholsterorlemia, polycystic kidney disease, hereditary

Cx phenotosterolemia polycystic kidney disease, hereditary

Cx phenotosterolemia polycystic kidney disease, hereditary

Cx phenotosterolemia polycystic kidney disease, thereditary

Cx phenotosterolemia polycystic kidney disease, thereofits

Cx altocimmune diseases, inflammation, cancer, diseases of the nervous

Cx system, infection by pathogenic microorganisms, and characteristics such

Cx altocimmune diseases, inflammation, cancer, diseases of the nervous

Cx system, infection by pathogenic microorganisms, and characteristics such

Cx altocimmune diseases, inflammation, cancer, diseases of the nervous

Cx system, infection by pathogenic microorganisms, and characteristics such

Cx altocimmune diseases, inflammation, cancer, diseases

Cx drugs or therapeutic treatments. The isolated polymorphic nucleic acid

Cx concert, diseases

Cx sequents or the repetitive or prophymorphic nucleic or prophylasis.
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                   different developmental stages, using the non-primate transcrift as probe is detected. A homologus gene having the same pattern of tit is used to identify the homologus human gene. The ESC transcripts it is used to identify the homologus human gene. The ESC transcripts identified by this method are used to generate transgenic animals selected from rats, hamsters, rabbits, dogs, pigs, horses, cows, monkey, babbon or chimpanzee for study of gene function. The method provides rapid and large scale screening for human developmental genes, and eliminates the need to analyse reporter gene expression in embryos. Sequence 86 BP; 16 A; 28 C; 30 G; 12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alana biallelic polymorphic DNA fragment EST98276a.

Human biallelic polymorphic DNA fragment EST98276a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologous non-human primate gene, in different cell types and/or at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                  Score 65.4; DB 1; Length 86;
Pred. No. 0.086;
0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9667 GCAATGGTCACCCGGCCTAGCAG 9689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prophylaxis of such diseases.
Sequence 100 BP; 21 A:
                                                                                                                                                                                                                                                                                                                                               0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17/c
X12087 standard; DNA; 100 BP.
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Best Local Similarity 77.00,
                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 80...
T2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1996; US-030455.
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05-NOV-1997; U20313
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22975 GTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCTGAAGAAGGAGGATCGCTTGAGTC 23034
                                                                                                                                                                                                                                                                                                                            30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment EST98276a.

Polymorphism: biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autolimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X12085 standard; DNA; 100 BP.
X12085;
30-MAL-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17731 TCAGCCTCCCAAATTGTTGGGATTACTAGTGTGAGTCAC 17769
                                                                                                 23035 CGGGAGTTCAAGAGCATCCTGGGCAACACAGCGAGACCC 23073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63.4; DB 1;
Pred. No. 0.17;
1; Mismatches 22;
                                                                                                                           05-NOV-1997; U20313.
06-NOV-1996; U3-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                               X12087 standard; DNA; 100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 76.8
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ID X1
AC X1
DT 30
                                                                                                                                                                                                                             RESULT
X12087
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Gaps

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21; Indels

1; Mismatches

Score 65; DB 1; Length 100; Pred. No. 0.099;

0.2%;

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

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Hudson 1, Landauder Es, wang D;
Hudson 1, Landauder Es, wang D;
Rew isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity
testing or phenotypic typing for disease
Claim 1; Page 218; 310pp; English.
X10269-X12937 are human DNA fragments which contain biallelic polymorphic
X10269-X12937 are human DNA fragments which contain biallelic polymorphic
X10269-X12937 are human DNA fragments which expresented in an expersa which have been isolated using the polymorphic site is indicated by
X09121-X10268. The base occupying the polymorphic site is indicated by
the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in
e.g. forensics, paternity testing or for phenotypic typing for diseases
Such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
hypercholesterolemia, polycystic Addeey disease, hereditary
spherocytosis, yon Willebrand's disease, tuberous scierosis, hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY 17671 GGGTCTTACTATGTTGCCCAGGCTGGTCTCAAACTCCTGGGCTTAAGTGATCCTCCTGCC 17730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drugs or therapeutic treatments. The isolated polymorphic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can also be used to produce medicaments for the treatment or x1s of such diseased. 25 C: 22 C: 20 C: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human biallelic polymorphic DNA fragment EST98276b.
Polymorphism; biallelic; human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Polymorphism; biallelic; human; forensic; paternity testing; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease testing or phenotypic typing for disease claim 1; Page 219; 310pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63.4; DB Pred. No. 0.17; 1; Mismatches
                                                                                                                                                                                                   14-MAX-1998.

05-NOV-1997; UZ0313.

06-NOV-1996; US-030455.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

Hudson T, Lander ES, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1998.
05-NOV-1997; UZ0313.
06-NOV-1996; UZ-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
Hudson T, Lander ES, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
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X12086;
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Best Local Similarity 76.8 Matches 76; Conservative
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WO9820165-A2.
                                                                                                                                               Homo sapiens.
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A1020 74.129; aten mindin Day languable, which collecting the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate UUPAC-TUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e-g. forensics, paternity testing or for phenotypic typing for diseases. In e-g. forensics, paternity testing or for phenotypic typing for diseases. In a sagammaglobulinemia, polyworthic syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous syndrome, osteogenesis imperfecta, acute intermittent porphyria, syndrome, diseases, inflammation, cancer, diseases of the nervous sa longevity, appearance (e-g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17671 GGGTCTTACTATGTTGCCCAGGCTGGTCTCAAACTCCTGGGCTTAAGTGATCCTCCTGCC 17730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9585 TCACTTGCCCTTGGCCTTGTGGTGACTCTCGGTCTTCTTAGGCAGAAGCACGGCCTGGAT 9644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGTCTTGCTATGTTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid fragment encoding gene products - can be used for genetic analysis and mapping Claim 1; Page 64; 616pp; English.

Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences exhibit no more than 90% homology to a human
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Brain; placenta; bone marrow; genetic analysis; gene mapping;
detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62.8; DB 1; Length 100;
Pred. No. 0.21;
); Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17731 TCAGCCTCCCAAATTGTTGGGATTACTAGTGTGAGTCAC 17769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TMAGCCTCCTAAAGTGCCAGGATTATAGGTGTGAGTCAC 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%; Score 63.4; DB 76.8%; Pred. No. 0.17; tive 1; Mismatches
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13-JUL-1992; GB-014857.
(MEDI-) MEDICAL RES COUNCIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Sequence 100 BP;
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WPI; 94-035056/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 76; Conserv
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Best Local Similarity
Matches 67; Conserv
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WO9401548-A.
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Query Match
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Hudson T, Lander ES, Wang D;

WPI; 98-286974/25.

New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity

T determining polymorphic forms for use in e.g. forensics, paternity

T esting or phenotypic typing for use in e.g. forensics, paternity

T esting or phenotypic typing for disease

S claim 1; Page 219; 310pp; English.

CC X10269-X12937 are human DNA fragments which contain biallelic polymorphic

CC X10269-X12937 are human DNA fragments which contain biallelic polymorphic

CC A10269-X12937 are human DNA fragments which contain biallelic polymorphic

CC A10269-X12937 are human DNA fragments which contains a indicated by

CC A10269-X12937 are human DNA fragments of a indicated by

CC A10269-X12937 are human DNA fragments of an individual for use in

CC A10269-X12937 are human DNA fragments in an individual for use in

CC Such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,

CC such as agammaglobulinemia, diabetes insipidus, Esch-Nyhan syndrome,

CC such as agammaglobulinemia, diabetes insipidus, Esch-Nyhan syndrome,

CC such as agammaglobulinemia, familial colonic polyposis, Bhiers Danios

CC sheer of the amportant familial colonic polyposis, Bhiers Danios

CC such as syndrome, osteogenesis imperfecta, acute intermittent porphyria,

CC autoimmune diseases, inflammation, cancer, diseases of the nervous

CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,

CC autoimmune diseases, inflammation, cancer, diseases, and characteristics such

CC A1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-X1020-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                       Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 TATAATCCCAGCACTTTTGGGAGGCCAAGGCAGACGGATCACTTGAAGTCAGGAGTTTGA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA, mRNA, relative abundance, frequency, human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Wossapiens. W09514772-A1.
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79.4%; Pred. No. 0.26;
Ive 1; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24436 GACTAGCCTGGCCAACATGATGAAACCCCATCTTCTACTAAAAATACA 24482
                                                                                                                                                                       X12095;
30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment TIGR-A003M18a.
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                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1997; U20313,
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T24892 standard; cDNA to mRNA; 100 BP
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Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prophylaxis of such diseases.
Sequence 108 BP; 19 A;
                                                                                                                           X12095/c
ID X12095 standard; DNA; 108 BP.
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Best Local Similarity 79.4%;
Watches 85; Conservative
9645 GTTAGGAAGGACGC 9658
                             14 GTTGGGCAGGACGC 1
                                                                                                                                                                                                                                                                                                            treatment; marker; ss
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9820165-A2.
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double-stranded DNA, which comprises one of the 7837 "GS" sequences double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which to able to hybridise to part of burnan genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3559 TTTTTTTTTTTGAGACGGAGTCTAGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCACCATC 3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 TIGITICITICAAACAGAGIGICACICIGICAGCCAGGCCGAGGCGAANGGIGCAATC 41
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                                                                                                                                                                e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.
                                                                                                                                                                                    CDNA that
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                                                                                                                                                   Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                             Claim 1; Page 1720; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recognising different cell types.
Sequence 100 BP; 28 A; 22
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hes 74; Conservative
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01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                          Okubo K;
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RESULT
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untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDRNs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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Sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
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                                                                                                                                                                                                                                                                                                        DB 1; Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 58.6; DB 73.7%; Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Human gene signature HUMGS08452.
                                                                                                                                                                                                                                                                                                                                                           73; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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Best Local Similarity
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Matches 74; Conserv
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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T25687 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the size of from various human tissues; synthesis of cDNA was initiated from the size of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end then all the 3'-oriented cobMAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 18 A; 23 G; 28 T;
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Human gene signature HUMGS08078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                       14-NOV-1996 (first entry)

Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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13806 TCTCGGCTCACTGCAACCTCTGCCTCCAGGGTTCTAGCAAT 13846
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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12-NOV-1993; JP-355504.
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Matsubara K, O)
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Matsubara K, Okubo K;

Matsubara K, Okubo K;

MPI; 95-206931/27.

Telentifying gene signatures in 3'-directed human cDNA library - e.g. dentifying gene signatures in 3'-directed human cDNA library - e.g. reflects relative abundance of corresp. mRNA in specific human rissues

Claim 1; Page 1942; 2245pp; Japanese.

A single-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T28637 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the siden of mRNA by using poly(T) as the sole primer. Since the 3'-curtanslated sequence; untranslated sequence Is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 84 BP; 33 A; 17 C; 15 G; 19 T;
  (MATS/) MATSUBARA K.
                              OKUBO K.
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ö 0; Gaps 0.2%; Score 56.4; DB 1; Length 84; 80.5%; Pred. No. 1.8; Live 0; Mismatches 16; Indels Query Match
Best Local Similarity 80.5°
Matches 66; Conservative

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Maximum DB seq length: 110
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1. .105
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_aref="taxon:9606"
/clone="Inb="Barstead colon HPLRB7"
/clone_lib="Barstead colon HPLRB7"
/sex=male"
/dev_stage="adult, age 25"
/lab_host="adult, age 25"
/lab_host="
                                                                                                                                                                                                                                                                                                                                                           3/]; double-stranded CDNA was ligated to Eco RI adaptors [5' AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R08388 95 bp mRNA EST 05-APR-1995
yf19d03.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:127301 5' similar to gb:M60750_cds1 HISTONE H2B (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High qality sequence stops: 68 Source: IMAGE Consortium, LLNL This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24533 AGGCTGAGGCAGGAGAATTGCCTGAACCTGGGAGGTGGAGGTTGCACTGAGCCAAGATCA 24592
                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGGTTGCGGTGAAGCCAAGATCG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY 24593 CACCATTGCACTCCAGCCTGGGCAACAAGAGCAAAACTCTGTCTC 24637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.8; DB 61;
Pred. No. 0.039;
); Mismatches 7;
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                                                                                                                                                  Location/Qualifiers
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Insert Size: 727
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nilarity 93.3%;
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 Contact: Wilson RK
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                                                                                             777382 yd72h12.r1
AA158786 zo63c11.r
AQ029690 RPCI11-41
AA44245 nC07a04.s
AA3535244 RPCI-11-3
AA703692 RPCI11-13
AA44252 zv68b02.r
AQ386882 RPCI11-13
AA44252 ax64b01.s
AA935205 ax64h01.s
A1991750 wt48e01.s
A1991750 wt48e01.s
B17434 345K2.rwb C
B17434 345K2.rwb C
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AQ544648 CITB1-E1-
AW196212 xm06e06.x
AA565533 nk42b11.s
AQ321855 RPCIII-11
AQ54648 CITB1-E1-
                                                                                                                                                                                                                                                                                                                                         AA811141 Ob48h02.5
AA443099 zr25h02.5
AA445299 zr26h02.7
AW083540 xc49f02.x
AW250394 2822460.3
AA228795 nc14e07.5
AQ076649 CIT-HSP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ544957 CITBI-E1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ260734 CITBI-E1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zo63c11.r
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B32951 HS-1016-A1-
B17434 345K2.TVB C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ062963 CIT-HSP-2
AA078003 7H12D08 C
AA218889 zq15d04.s
                            AI832832 at72g09.x
                                               R08388 yf19d03.rl
AI832832 at72g09.x
AA807640 nx08b05.s
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AA654562 nt75f10.s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vw52c09.s1
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 105)

Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lery,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashUnKI human EST Project

Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133644.
Description
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AQ321855
AQ544648
AA250812
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AW196212
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AA703692
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AA807640
T77382
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AI991750
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AA897366
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B65160
AA812141
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AW083640
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AA654562
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IMAGE:2377600 3' similar to contains Alu repetitive
element; contains element MER22 repetitive element; mRNA sequence.
AI832832. GI:5454812
clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 727 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 68.
Location/Qualifiers
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1 (bases 1 to 105)
11 (bases 1 to 105)
12 (bases 1 to 105)
13 (bases 1 to 105)
14 (bases 1 to 105)
15 (bases 1 to 105)
16 (bases 1 to 105)
17 (bases 1 to 105)
18 (bases 1 to 105)
19 (bases 1 to 
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                            /db_xref-"taxon:9606"
/clone-"IMAGE:127301"
/clone_lib-"Soares fetal liver spleen INFLS"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92; DB 21; Length 95;
Pred. No. 0.067;
0; Mismatches 3; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
En (Confer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Indubilished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151346.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@hlh.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Consultation information can be found through the I.M.A.G.E. Consortium/LiNI. at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                    /clone="INAGE:2377600"
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/sex="male"
/dev_stage="adult, age 25"
/dev_bost="blub (phage resistant)"
/lab_host="blub resistant"
/lab_host="blub (phage resistant)"
/lab_host="blub (phage resistant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 0.061;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ay 12214 GCAACCTCCGCCTCCCGGGTTCAAGCCATTCTCCTGCCTCAGCCT 12258
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/db_xref="taxon.9606"
/clone="IMAGE:1255473"
/clone="Lib="NCI_CGAP_GC3"
/tissue_type="pooled_germ_cell_tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 774 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
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AA807640.1 GI:2877108
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Email: estewatson.wustl.edu
Insert Size: 943
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Putative full length read
Insert Length: 943 Std Error: 0.00
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT/T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer: Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777382 103 bp mRNA EST 15-MAR-1995
yd72h12.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:113831 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3734 AGTAGAGATGGGGTTTCACCGTGTTAGCCAGAACGGTCTCGATCTCTTGACCTTCTGATC 3793
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Lew., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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0
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Other_ESTs: yd72h12.s1
Contact: Wilson RK
Washington University School of Medicine
14444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                 Score 87.6; DB 38; Length 103;
Pred. No. 0.21;
0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:113831"
/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3794 CGCCTGCCTTGCCTTCCCAAAGTGCTGGGATTACAGGTGTGA 3835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CGCTCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGA 103

    103
/organism="Homo sapiens"
/db_xref="GDB:469448"

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High quality sequence stop: 109.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T77382.1 GI:694585
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T77382/c
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KEYWORDS
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zo63c11.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:591572 5' similar to contains Alu repetitive element; contains element PTR7 repetitive element;, mRNA sequence.
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1 (bases 1 to 106)

11.11.1er, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, C., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
On Depublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406940.
                                                                                                                                                                                                                                                                                     6073 TGAGAGTCTCACTCTCACTGCAACCTCCCCCTCCTATATTCAAGTGATTCTCTTGCCTCA 6132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 119
Insert Length: 926 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           103 TGAGAGTCTCACTCTCACTCACCCCCCCCCCTATATTCAAGTGATTCTCTTGCCTCA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                            Score 86.6; DB 21; Length 103;
Pred. No. 0.28;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                             6133 GCCTCCCGAGTAGCTGGGACTACAGGCGTGCAC 6165
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Matches 89; Conserv
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AA158786/c
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49 TACTAAAACTACAAAATTAGCCGGGCATGAAGGAGCATGACTGTAATC 1
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TITLE
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                                                                                                                                                     ACCESSION
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KEYWORDS
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El (bases 1 to 109)
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
L Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdddams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
                                                                                                                                                                                                                                                                                                                       AQ029690 109 bp DNA GSS 14-APR-1999
RPCI11-41F18.TV RPCI-11 HOMO sapiens genomic clone RPCI-11-41F18,
                                                                                                             12168 CTCTTGTTTCCCAGGCTGGAGTGCAATGGCGGTCTTGGCTCACAGCAACCTCCGCCTC 12227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4703 CATATCACCTGAGGTCAGGAGTTTGAGACCAGGCTGGCCAACATGGTGAAACCCTGTCTC 4762
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                                                                           Gaps
                                                                                                                                 104 CTCTTGTTGCCCAGGCTGGAGTGCAATGGTGCGACCTTGGCTCACTGCAACCTCCGCCTC 45
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                                     Length 106;
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                                                                                                                                                                                                             DB 29;
                                                                         12;
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Pred. No. 0.42;
0; Mismatches
                                                     0.45;
                                   Score 84.8; D
Pred. No. 0.45
0; Mismatches
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/db_xref="taxon:9606"
/clone="RPCI-11-41F18"
/clone_lib="RPCI-11"
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1. .109
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AQ029690.1 GI:3274821
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ilarity 88.5%;
Conservative
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Best Local Similarity 86.2%
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                                   Query Match
Best Local Similarity
Matches 92; Conserv
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AQ029690/C
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Tumor Gene Index

Unpublished (1997)

On Jan 24, 1995 this sequence version replaced gi:634306.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Kirzman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 110)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA244245 110 bp mRNA EST 20-AUG-1997 nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence.
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26 c 28 q 38 t.
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Pred. No. 0.42;
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/db_xref="taxon:9606"
/clone="IMAGE:1007406"
/clone_llb="NCI_CGAP_Pr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="45 years old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 90. Location/Qualiflers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / ncce="Organization" or provided by the provided by the modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHIJ9W, testis NHT, and B-cell NCL_CGAP_CGED) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 ilbraries. The pools consisted of I.M. A.G.E. clones 227480-302087, 682632-667239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 27 c 29 g 32 t
                                                                                                                                                                                                                                                                                                       Tumor Gene Index
I Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150764.
On Jan 19, 1998 this sequence version replaced gi:2150764.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenh, gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 834 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 63.
Location/Qualifiers
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                   AA897366 110 bp mRNA EST 04-JAN-1999 am06h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466067 3' similar to contains Alu repetitive element;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
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86.2%; Pred. No. 0.42;
tive 0; Mismatches 15; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:1466067"
/clone=lb="Soares_NFL_T_GBC_S1"
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                                                                                                         AA897366
AA897366.1 GI:3033986
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AQ535244.1 GI:4846934
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Matches 94; Conservative
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Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact Canomics
The Institute for Genomics
The Institute of Genomics
Tel: 301 838 0200
Fax: 30
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (basea 1 to 106)

Hillider,L., Allon,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,C., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1397630.

Contact: Wilson RK
Washington University School of Medicine
1 (bases 1 to 103)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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/db_xref="GDB:7621533"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11"
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E (Dasses 1 to 110)

S Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)

Cottact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
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                                                                                                                                                                                                  Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ386882 110 bp DNA GSS 21-MAY-1999
RPCIII-13414.TV RPCI-11 HOMO sapiens genomic clone RPCI-11-13414,
                                                 Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.53;
0; Mismatches 13; Indels 0,
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AQ386882.1 GI:4357905
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Best Local Similarity 87.6%;
Matches 92; Conservative 0
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Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 110)

S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Monce,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Washu-Nerck EST Project 1997

L Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1400965.

Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                           /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
of c 38 g 20 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     8172 GGCCGGGCGCGCGCTCACGCCTGTAATCCCAGCACTTTGGTAGGCAGAGGCTGGCGGA 8231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Scares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
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85.5%; Pred. No. v...
0; Mismatches
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/db_xref="taxon:9606"
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/db_xref="GDB:7551267"
                                                                         /clone="RPCI-11-13414"
/clone_llb="RPCI-11"
/sex="Male"
                                                    /db_xref="taxon:9606"
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AA442529.1 GI:2154407
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                                                                                                                                                                                                                  ô
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 27 c 32 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ak64h01.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone MAGE:1412689 3' similar to contains Alu repetitive element; contains element KER repetitive element; , mRNA sequence. AA835205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Onpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:636191.
                                                                                                                                                                                                                                                       12153 TGAGACGAAGTTTCTCTCTTGTTTCCCAGGCTGGAGTGCAATGGCGCGATCTTGGCTCAC 12212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoelmage.llnl.gov) for further information.
Seq primer: -40ml3 from Amersham.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                          Score 84; DB 33; Length 110;
Pred. No. 0.55;
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1412689"
/clone_lib="Barstead pancreas HPLRB1"
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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ilarity 86.1%;
Conservative
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Tunor Gene Index
Unpublished (1997)
On Doc 20, 1995 this sequence version replaced gi:1133359.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally, Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butherla: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                            3569 TGAGACGGAGTCTAGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCACCATCTTGGCTCACT 3628
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    DB 39;
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  Score 83.4; DB
Pred. No. 0.67;
0; Mismatches
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/organism="Homo sapiens"
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/clone="IMAGE:2510712"
/clone=lib="NCI_CGAP_Pan1"
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High quality sequence stop: 62.
Location/Qualifiers
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AI991750.1 GI:5838578
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Search completed: June 17, 2000, 20:31:38 Job time: 287665 sec

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Sequence Seq

Sequence 3 Sequence 3 Sequence 3 Sequence 5 Sequence 5 Sequence 5

Sequence Sequence

ALIGNMENTS

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CZHY: 94240

CZHY: 94240

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC - COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTONEY/AGENT INFORMATION:
NAME: Lauder: Leona L.
RECISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
REFERENCE/DOCKET NUMBER: BO 0221.3E
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-00-481-658B-65
Sequence 65, Application US/08481658B
SPECHOR NO. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leona L. Lauder
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INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
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CITY: Tiburon
STATE: California
COUNTRY: USA
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/cgn2_6/ptodata/1/ina/6_COWB.seq:*
/cgn2_6/ptodata/1/ina/pcrus_COWB.seq:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-477-504A-65
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US-08-477-504A-65
US-08-486-756A-65
US-08-485-862B-65
US-08-485-862B-65
US-08-485-862B-65
US-08-487-865B-65
US-08-739-65
US-08-739-65
US-08-739-65
US-08-757-70
US-08-45-77-70
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US-08-45-67-69
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PCT-US95-17111A-91
US-08-454-557C-91
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 110
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Match 1
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Length 105;

Score 69.8; DB 4; Pred. No. 9.6e-07;

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US-08-477-504A-65
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                                      3720 TTTTTTTTTTTTTAGTAGAGATGGGGTTTCACCGTGTTAGCCAGAACGGTCTCGATCTC 3779
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22; Indels
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                                                                                                                                       61 CTGACCTTGTGATCCACCCTCGGCCTCCCAAAGTGCTGGGAT 105
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  0; Mismatches
                                                                                                                                                                                                                                                                                                                  APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ATTLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PETENTIN MERRIN APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION A424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAUGA: LEONER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECHONE: 415-435-2034
TELECHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     US-08-481-658B-65/c
; Sequence 65, Application US/08481658B
: Datent No. 5955075
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
83; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
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US-08-481-658B-65
  Matches
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3720 TITITITITITATITAGIAGAGAIGGGGTITCACCGIGIIAGCCAGAACGGICICGAICIC 3779
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Pred. No. 9.6e-07;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ANTORIET APPLICATION:
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDEMESS: 86
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
Sequence 65, Application US/08477504A
Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFRENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                      Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.2%;
Best Local Similarity 79.0%;
Matches 83; Conservative
                                                                                                                                                                                                                                       6 Mariposa Court
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. 1
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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CITY: Tiburon
STATE: Californ
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US-08-477-504A-65
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RESULT

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CLASSIFICATION:
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85.6%; Pred. No. 1.1e-06;
Live 0; Mismatches 14; Indels
                                                                          COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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PAPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
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Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
APPLICANT: Astore
COUNTRY: Liburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                      NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/477,504A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDYTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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Matches 89; Conservative
                   California
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Tiburon
                                         USA
                                                          94920
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US-08-477-504A-65
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                                         COUNTRY:
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3720 IIIIIIIIIIIIAIIIAGIAGAGAIGGGGIIICACCGIGIIAGCCAGAACGGICICGAICIC 3779
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION WHER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAUGH: Laugh: Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3780 TIGACCTTCTGATCCGCCTGCCTTGGCTTCCCAAAGTGCTGGGAT 3824
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APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TTTLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: G Mariposa Court
CITY: Tiburon
STATE: California
                                                                                            NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/COCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERSTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 65, Application US/08486756A
; Patent No. 5981711
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TELEPHONE: 415-435-2034
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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Matches 83; Conserv
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US-08-486-756A-65
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.2%; Score 69.6; DB 4; Length 105; Best Local Similarity 85.6%; Pred. No. 1.1e-06; Matches 89; Conservative 0; Mismatches 14; Indels
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Patent No. 5989838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Janomir
TITLE OF INVENTION: MN Gene and Protein
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: G Mariposa Court
CITY: Tiburon
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                   LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
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                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
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HYPOTHETICAL: NO
NS-08-486-756A-65
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US-08-485-862B-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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Score 69.8; DB 4; Length 105;
Pred. No. 9.6e-07;
0; Mismatches 22; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk
COMPUTER: BLAB FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: BRABCH FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 0'-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 08/477,504
FILING DATE: 0'-JUN-1995
APPLICATION NUMBER: US 08/477,504
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: LEONAL LEONAL
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                                                                                                                                                                                                                                                                                                                                    3780 TIGACCTICTGATCCGCCTGCCTTGGCTTCCCAAAGTGCTGGGAT 3824
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85.6%; Pred. No. 1.1e-06;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 65, Application US/08485862B
; Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
        0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6 Mariposa Court
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nucleic acid
                                              Best Local Similarity 79.0
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 89; Conserv
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-485-862B-65/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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US-08-485-862B-65
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3720 TITITITITITATITAGTAGAGAIGGGGTTTCACCGTGTTAGCCAGAACGGTCTCGATCTC 3779
                                1 ITITITACATCITIAGIAGACAGGGTTCACCATATIGGCCAGGCTGCTCTAAACIC 60
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,739

FILING DATE: 24-JAN-1997

PRIOR APPLICATION NUMBER: US 08/485,049

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/486,756

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/486,756

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/481,656

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/481,658

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/485,862

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/485,863

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/485,863

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/485,863

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/487,077

FILING DATE: 07-JAN-1995

PRIOR APPLICATION NUMBER: US 08/487,077

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/487,077

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/487,077

FILING DATE: US-JUN-1995

APPLICATION NUMBER: US 08/487,077
                                                                                                        3780 TIGACCTICIGATCCGCCTGCCTTGGCTTCCCAAAGTGCTGGGAT 3824
                                                                                                                                61 CTGACCTTGTGATCCACCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-0021.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   RESULT 10
US-08-787-739-65/c
: Sequence 65, Application US/08787739
: Patent No. 6027887
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TELEPHONE: 415-981-2034
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lauder, Leona L. REGISTRATION NUMBER; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        잁
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US-08-787-739-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICA DATE: 24-04M-199/
PRICATION DATA:
APPLICATION DATA:
FILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                    E: Leona L. Lauder
369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94104
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     US-08-787-739-65
Sequence 65, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-0332
TELEFAX: 415-981-0332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.2
Best Local Similarity 79.0
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 369 Pine Stre
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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GENERAL INFORMATION:
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APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: De Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2840 GCCCAGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACTATGTTGGCCCAGGCTAGT 2899
                                                                                                         1393 ATCTCAGCACTTTGGGAGGCTGAGG-GCACAGATCACGAGGTCGGGAGTTTGAGACCAGC 1451
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                                                                                                                                                  105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
                                                                  Gaps
                                                                1;
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                      Length 105;
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                                                             14; Indels
                                                                                                                                                                                                1452 CTGGCCAATATGGCGAAACCCTGTCTTCTACTAAAAATACAAAA 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWALTER PATENTIN Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FLING DATE: 30-MAY 1995
CLASSIFICATION: 514
ATTONNEY/AGERT INFORMATION:
NAME: LIGHAIO, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/POCKET UNBER: 36,203
REFERENCE/COCKET UNBER: 0609.3840003
TELECOMMULCATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHRARCTERISTICS:
LENTH: 78 base pairs
                                                                                                                                                                                                                                         45 CTGGCCAATATGGTGAAACCCTGTCTTACTAAAAGATGTAAAAA 2
                  0.2%; Score 69.6; DB 5;
85.6%; Pred. No. 1.1e-06;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 70, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/08454557C Patent No. 5830670
                Query Match 0.23
Best Local Similarity 85.65
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2900 TTGGAACTCCTGA 2912
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US-08-454-557C-70
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Patent No. 5948888
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION:
TITLE OF INVENTION: Allaheimer's Disease
TITLE OF INVENTION: Allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
APPLICANT: de la Monte, Suzanne
PAPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2840 GCCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTAGT 2899
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                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILLNG DATE: 14-NOV-1994
CLASSIFICATION: 435
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Pred. No. 0.00025;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lidwig, Steven R.
REGISTRATION UNDHER: 36,203
REFERENCE/DOCKET UNDHER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 371-2600
TELEFRAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Best Local Similarity 87.7%;
Matches 64; Conservative
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LENGTH: 78 base pairs
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                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
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OPERATING SYSTEM:
                                                                                                                                                                  STREET: 1100 New CITY: Washington
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Indels

Score 58.6; DB 6; Pred. No. 0.00025; 0; Mismatches 9;

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2840 GCCCAGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTAGT 2899
                                                                                                                                                                                                        6 GCCCAGCTAATATTTGTATTTTTAGTAGATGGGGTTTCTCCATGTTCATCAGCTGGT 65
                                                                                      Query Match 0.2%;
Best Local Similarity 87.7%;
Matches 64; Conservative (
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US-08-454-557C-70/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & FOX P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STRATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-1934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Plan PC compatible
COMPUTER: Plan PC compatible
COMPUTER: Plan PC compatible
COMPUTER: PLAN PC COMPATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 78;
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87.7%; Pred. No. 0.00025;
tive 0; Mismatches 9;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNET/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAS: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
           PPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 300
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.;
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-240
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
US-08-450-673C-70
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.2%
Best Local Similarity 87.7%
Matches 64; Conservative
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LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
CURRENT APPLICATION DATA:
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PCT-US95-17111A-70
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Sequence 70, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1433 TCGGGAGTTTGAGACCAGCCTGGCCAATATGGCGAAACCCTGTCTCTACTAAAAATACAA 1492
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STREET: 1100 New York Avenue, Suite 600
CITX: Washington
                                                                                                                                                                                                                                                       CITI:
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
TITING DATE: 30-MAY-1995
TITING DATE: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.2%; Score 57.2; DB 3; Best Local Similarity 83.3%; Pred. No. 0.00051; Matches 65; Conservative 0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
REFRENCE/COCKET NUMBER: 0609,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR ESO ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDENESS: both
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq length: 110
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Perfect score:
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gb_pt3: *
gb_htg8: *
gb_htg9: *
gb_htg11: *
gb_htg11: *
gb_htg12: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 2
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VERSION
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KEYWORDS
SOURCE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96)
Lauer,P., Meyer,N.C., Prass,C.E., Starnes,S.M., Wolff,R.K. and
                                     sy899g1-19 Human (A.Gnirke) Homo sapiens STS genomic, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                         29-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                      92 degrees C for 20 seconds 60 degrees C for 45 seconds 72 degrees C for 60 seconds 75
                                                                                                                                                                                                                                                                                Confact: Andreas Gnirke
Mercator Genetics, Inc.
4040 Campbell Ave, Menlo Park CA, 94025, USA
Email: gnirke@mercator.com
Primer A: GTCCCCAAGAATAAATGAG
Primer B: AGGGCACAGGGAAG
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each 0.8 uM
each 200 uM
0.05 units/ul
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0.001% (w/v).
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    .96
    /organism="Homo sapiens"
/db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5 mM
50 mM
10 mM
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23 g
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                                                                                                                                                                                                                                                                                                                                                                                                   Annealing:
Polymerization:
PCR Cycles:
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                        PCR Profile:
Denaturation:
                         dq 96
                                                                          G31304.1 GI:1871333
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Best Local Similarity 99.04
Matches 95; Conservative
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 108)

1. (bases 1 to 108)

1. Miliamson, R. and Humphries, S.

1. Williamson, R. and Humphries, S.

1. Miliamson, R. and Humphries, S.

1. Blochem. 164 (1), 77-81 (1987)

2. Eur. J. Blochem. 164 (1), 77-81 (1987)

3. See X05252 for deletion junction

Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.

1. Location/Qualifiers
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Meisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-likoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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   20-MAY-1992
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                                                                                                                    Alu repetitive sequence; low density lipoprotein receptor
HSLDLRN2 108 bp DNA PRI 20-MAY-
Human LDL-receptor gene intron 14 fragment (normal gene).
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Human LDL-receptor gene intron 14 fragment (normal gene)
X05250
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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91.5%; Pred. No. 1.4e-07;
ative 0; Mismatches 9;
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/db_xref-"taxon:9606"
1. 108
/note="intron XIV fragment"
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23 c 39 g 18 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                            GI:34337
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Matches 97; Conservative
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (12-840-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OY 10859 TAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCA 10918
                                                                                                      7126 AAAAAACTTAGCCGTGCATGGTGGCATGCGCCTGTAGTCTCAGCCACTTGGGAGGCTGAG 7185
                                                                            Gaps
                                                                                                                       Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eukheria, Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 108)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M. A. and Deininger, P. L.
CDNAs derived from primary and small cytoplasmic Alu (scalu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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                                           Length 108;
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Homo sapiens male embryo carcinoma cDNA to other RNA
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                                                                                                                                                                    7186 GCAGGAAAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAG 7233
                                                                                                                                                                                   61 GCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAG 108
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Pred. No. 6.7e-07;
                                                                           12;
                                            DB 10;
                                         Score 88.8; DB 10
Pred. No. 4.7e-07;
0; Mismatches 12
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Human small cytoplasmic Alu transcript.
U67803
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/db_xref-"taxon:9606"
/clone-"TscAlu2"
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/rpt_type=dispersed
39 c 30 q
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/note="scAlu"
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Best Local Similarity 94.8%;
Matches 91; Conservative
                                         tch 0.3%;
al Similarity 88.9%;
96; Conservative
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HUMALCE162/c
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitsed (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10688 TTTTTGGGGTGGGGTCTCGTCACCTAGGCTGGAGTGCAGTGGCGCAAACTCGGC 10747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87; DB 9; Length 107;
Pred. No. 1e-06;
0; Mismatches 10; Indels
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Human small cytoplasmic Alu transcript.
U67804
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
/tissue_type="carcinoma"
a 30 c 35 g 14
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/db_xref="taxon:9606"
/clone="TscAlu3"
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/rpt_type=dispersed
38 c 26 q
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Best Local Similarity 90.39
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Matches 90; Conservative
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/tissue\_type="carcinoma"

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Query Match
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1 (bases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of
10860 AGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCAC 10919
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896, GI:174874
                                                                                                                                                                                          HUMALCE221 103 bp ss-RNA PRI 15-APR-199.
Human carcinoma cell-derived Alu RNA transcript, clone CE221
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                       post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
Location/Qualifiers
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89.3%; Pred. No. 2.1e-06;
tive 0; Mismatches 11;
                                                                   10920 CCGCTTTGGCCTCCCAAAGTGCTGGGATTACAGGC 10954
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 g 1
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/db_xref="taxon:9606"
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/dev_stage="embryo"
/sex="male"
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/sex="male"
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Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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                                                                        , 3.8e-06;
10; Indels
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Pred. No. 3.5e-06;
0; Mismatches 13
                                                                                                                 Pred. No. 3.8e-
0; Mismatches
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                                                                                              Score 84;
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1. 108
/note="intron XII fragment"
a 38 c 20 g 29 t
      /note="Alu repeat"
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HSLDLRD2
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HSLDLRD1/c
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Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,

Williamson, R. and Humpfries, S.

Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Bur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                      See X05250 for corresponding normal gene sequence. In the defective LDL-receptor gene the deletion ocurred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
                                                                                                                                                    Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="blood leukocytes from a patient with familial"
1. .108
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
density lipoprotein.
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
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Alu repetitive sequence; low density lipoprotein receptor;
repetitive sequence.
                    Alu repetitive sequence; low density lipoprotein receptor
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.2; DB 10;
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0; Mismatches 13
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20 c 40 g 20 t
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
complement(<1..65)
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ilarity 87.6%;
Conservative
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Best Local Similarity
                                                            Homo sapiens
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Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;

Primates; Catarrhil; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,

Williamson, R. and Humphries, S.

Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
allu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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                                                                                                                      5414 TCGGCTCACCGCAACCTCTACCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGA 5473
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                                                                                                                                                      2 TCGCCTCACCACCACCTCTGCCTCCTGGGTTCAAACCATTTTCCTGCCTCAGCCTCTA 61
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0.3%; Score 81.4; DB 10; Length 108; 85.0%; Pred. No. 1.2e-05;
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85.0%; Pred. No. 1.2e-05;
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27
                                           repeat_region
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Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                              Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. Milliamson, R. and Humphries, S. Olnequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Burect Submission
Submitted (12-406-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
Human LDL-receptor mutated gene with intron 14 deletion junction.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
Shaikh, T. H., Roy, A. M., Klm, J., Batzer, M. A. and Deininger, P. L.
CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
                                                          Alu repetitive sequence; low density lipoprotein receptor
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Pred. No. 1.2e-05;
0; Mismatches 16;
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Human small cytoplasmic Alu transcript.
U67808
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                                     X05251.1 GI:34336
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
Sinnett.D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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Human carcinoma cell-derived Alu RNA transcript, clone CE43.
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                                                                                                                                                                                                                                   10; Indels
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Pred. No. 3.7e-05;
0; Mismatches 17;
                                                                                                                                                                                            DB 11;
3.4e-05;
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                                                                                                                                                                                            Score 79; DB :
Pred. No. 3.4e of Mismatches
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/db_xref="taxon:9606"
/dcll_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
                                                                                                                 21
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31 c 34 q 1
/db_xref="taxon:9606"
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                                                                    /rpt_family="Alu"
/rpt_type=dispersed
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                  /clone="TscAlu7"
                                    1. .108
/note="scAlu"
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84.0%;
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Best Local Similarity 89.5%;
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Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                     05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
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Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Homo sapiens.
                                                                        24892 standard; cDNA to mRNA; 100 BP
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24-JUL-1996 (first entry)
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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double-stranded DNA, which comprises one of the 7837 "GS" sequences double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mNAM is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was inlitated from the 3'-end of mNAM by using poly(T) as the sole primer. Since the 3'-tuntranslated sequence; unitanslated sequence is unique to a particular mNAM species, almost all the 3'-oriented cDNAs hybridise with specific mNAMs. Each library is constructed so as to reflect accurately the relative abundance of different mNAMs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                            100 CATGGAGAAAATACTGTCCCTACTNAAAATCAACTGGCTGGACATGGTGGCACACAC 41
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for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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0.036;
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                                           Claim 1; Page 758-759; 2245pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 78; Conserv
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Not claim it Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic x10269-X12937 are human DNA fragments which perimers represented in contain the paper of the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in contain a sagammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, contours as anomaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, contours dystrophy, Wiskott-Aidrich syndrome, rebry signatury dispersorbasterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary contourned is claiming contour polyposis, Ehlers-Danios syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous contour infection by pathogenium acute intermittent porphyria, appropriate the part of the par
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isolated polymorphic nucleic acid
                                                  segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases. Sequence 108 Bp; 19 A; 23 C; 28 G; 37 T;
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Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autotimnue disease; cancer; inflammation; drug; therapy; medicament.
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                                                                                                                                                                                                                                                                                                DB 1; Length 108;
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Pred. No. 0.072;
1; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TTCAAGTGATCCGTCTGCCTTGCCTCCCAAAGTGCTGGGATTATAG 108
                                                                                                                                                                                                                                                                                      Score 65.2; DB 1; Length 1
Pred. No. 0.047;
1; Mismatches 19; Indels
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     drugs or therapeutic treatments. The
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                                                                                                                                                                                                                                                                                      0.2%;
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X12086 standard; DNA; 100 BP.
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Best Local Similarity 77.6%;
Matches 76; Conservative
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                                                                                                                                                       19 A;
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                                                                                                                                                                                                                                                                                      Query Match 0.29
Best Local Similarity 80.69
Matches 87; Conservative
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
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determining polymorphic forms for use in e.g. forensics, paternicy determining polymorphic typing for disease

Claim 1. Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in markers which have been isolated using the primers represented in markers which have been isolated using the primers represented in care appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in caton a sagammagalobulinmanta, diabetes insiphdua, feach Nyhan syndrome, cuch as agammagalobulinmanta, diabetes insiphdua, feach Nyhan syndrome, papercholesterolemia, polycystic kidney disease, hereditary hamorrhagic telangiectasia, familial colonic polyposis, Bhiers-banlos syndrome, osteogenesis imperfecta, acute intermittent porphyria.

Syndrome, osteogenesis imperfecta, acute intermittent porphyria, autolimune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid grugs or therapeutic treatments. The isolated polymorphic or correspondence.
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Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                         Human bialielic polymorphic DNA fragment EST98276a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining polymorphic forms for use in e.g. forensics, paternity
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1; Mismatches
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                                                                                   (first entry)
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                           standard; DNA; 100
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Matches 75; Conservative
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
                                                                                                                                                                                                                                    treatment; marker; ss
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Sequence 100
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WO9820165-A2.
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WO9820165-A2.
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87/c
x12087 a
x12087;
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X12087
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4261 GTGGCTCACGGCTGTAATCCCAGCACTTCAGGAGGCTGAGTTGGGGAGAATCGCTTGAGCT 4320

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99 GTGACTCACACCTATAATCCTGGCACTTTAGGAGGCTKAGGAAGGAGGATGTTTGAAAC 40

4321 CAGGAGTTCAAGACCATTTTGGGCAACATAGCAAGTCT 4358

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Query Match
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                                                                             While year Sangery A.2.

New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity resting or phenotyphic typing for disease

Election 1, Page 218; 310pp; English.

Claim 1, Page 218; 310pp; English.

Claim 1, Page 218; 310pp; English.

Claim 1, Page 218; 310pp; English.

CC markers which have been isolated using the primers represented in the perpendicular of the perpendicular of the primers represented in the control of the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the complex for determining polymorphic forms in an individual for use in the code of as agammagiobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, code as agammagiobulinemia, diabetes insipidus, Easch-Nyhan syndrome, such as agammagiobulinemia, polycystic kidney disease, hereditary spherorolesterolemia, polycystic kidney disease, colonic polyposis, Ehers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid copyphylaxis of such diseases.

C prophylaxis of such diseases.

Sequence 100 BP; 22 A; 25 C; 22 G; 30 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                                                     Hudson T, Lander ES, Wang D;
WPI: 98-286974/25.
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Matches 75; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                  US-030455.
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05-NOV-1997; U20313
06-NOV-1996; US-030
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01-JUN-1995.
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T24892
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences could be stranded DNA) which comprises one of the 7837 "GS" sequences obtained from 3'-directed cDNA libraries prepared from arious human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-entranslated sequence is unique to a particular mRNA species, almost untranslated course of the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 21 C; 25 G; 23 T;
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3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

22 C; 25 G; 22 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene signature HUMĠŚ08452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying gene signatures in 3'-directed human cDNA library-for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6324 CCTGGGAGACAGGGCGAGCTCCGTCTCGAAAAAAAAAA 6362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CCTGGGTGACAGAGTGACATCTGTTTGAAACAAAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T26213 standard; cDNA to mRNA; 103
                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.2
Best Local Similarity 75.8
Matches 75; Conservative
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Matches 77; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okubo K;
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CDNA that

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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA hibraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-entranslated sequence is unique to a particular mRNAs pecies, almost is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 99 BP; 43 A; 18 C; 16 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15706 CAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCACTCTATCACC 15765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 758-759; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
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Gene signature: messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp, mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.49
Watches 70; Conservative
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11-ROV-1994; J01916.
12-ROV-1993; JP-355504.
(MAYES) MATSUBARA K.
(OKUB/) OKUBC K.
12-NOV-1993; JP-355504
                                                                          Okubo K;
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                     (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                          Matsubara K, Okub
WPI; 95-206931/27.
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T20927
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                                                                                                                                                                                                                                            14-NOV-1996 (first entry)

Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsubara K, Okubo K;
WPI: 95-206931/27.
Tdentlifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                     Qy 15789 TCTCAGCTCACTGCAACCTGCACCTCCTGGGTTCAAGGGAT 15829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy 10957 GAGCCACCGTGCCCGGCCTACTTCATTTCATTTAAAA 10997
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                                                  numuan; cloning; mapping; non-biased libr
cell typing; abnormal cell function; ss.
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Claim 1; Page 2182; 2245pp; Japanese.
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ID T20931 standard; cDNA to mRNA; 99 BP.
                                                                                                                                                                                                    T26828 standard; cDNA to mRNA; 108
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Human gene signature HUMGS02184.
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Best Local Similarity 75.2
Matches 76; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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01-JUN-1995.
11-NOV-1994; J01916.
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                                                                                                                                                                                                                                  21738 ATTCTCCTGCCTCAGCCTCCCAAGCAGCTGGGATTACAGGTACCTGCCACCATGCCTGGT 21797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "Gs" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was delived.
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                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                    2 ATCCTCCCACTTCCACCTCCCAAGTAGCTGTGGCTACAGGTGTGTGCCACCATGTCCAGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
is constructed so as to reflect accurately the relative abundance of different marks in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 27 C; 21 G; 31 T;
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Sequence 91 BP: 18 A: 22 C; 28 G; 18 T;
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Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                             DB 1; Length 103;
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                                                                                                                                                                                              25; Indels
                                                                                                                                                                                                                                                                                                      Qy 21798 TAATTTTTGTATTTTTAGTAGAGGGGGTTTCACCATG 21836
                                                                                                                                                                                                                                                                                                                          Query Match 0.2%; Score 60.2; DB Best Local Similarity 74.7%; Pred. No. 0.28; Matches 74; Conservative 0; Mismatches
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Claim 1; Page 1944; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                             T25854 standard; cDNA to mRNA; 91 BP
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Human gene signature HUMGS08084.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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Matches 69; Conserv
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A single-stranded DNA) which complementary strand or the corresp.

A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences.

G given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3 '-directed cDNA hibraries prepared from various human tissues; synthesis of CDNA was initiated from the 3 '-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed as oas to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
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                                                                                                                                                                           14-NOV-1996 (first entry)

Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
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83.5%; Pred. No. 0.37;
vative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2182; 2245pp; Japanese.
30 TGAACCNCTGCCTCCTAGGCTCAAGTGAT
                                                                                                                             T26828 standard; cDNA to mRNA; 108
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Human gene signature HUMGS07131.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MAYEZ) MATSUBARA K.
(OKUB/) OKUBO K.
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Claim 1; Page 1748; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

Couble-stranded DNA, which comprises one of the 7837 "65" sequences

Given in T19001-T26837 and which is able to hybridise to part of

human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)

sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

circum various human tissues; synthesis of cDNA was initiated from the

circum various human poly(T) as the sole primer. Since the 3'-

untranslated sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS

recognising different cell types.

Sequences) as a means of diagnosing abnormal cell function or for

recognising different cell these.
Matsubara K, Okubo K;
WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                          tissues
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ö 15723 TTTTTTTTTTTTTTTTTGAGACAGAGTCTCACTCTATCACCCAGGCTGGAGTGCAGG 15782 0; Gaps Query Match 0.2%; Score 58.6; DB 1; Length 108; Best Local Similarity 71.0%; Pred. No. 0.49; Matches 76; Conservative 0; Mismatches 31; Indels ( ò

108 TITGHITGTIGITGTIGITTTCAACAGGGTCTTGCTCTGTGTCAGGCTGGAAINCAGTG 49

OY 15783 GCACAATCTCAGCTCACTGCAACCTGCACCTCCTGGGTTCAAGGGAT 15829

Search completed: June 18, 2000, 10:13:39 Job time: 335730 sec

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1 GATAATTATTTAATATTAT.....ACCCTTTGATGAGAACATGA 29001
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AA442529 zv68b02.x
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AA226656 nc19f09.s
AQ062963 CIT-HSP-2
AA897366 am06h02.s
AQ003188 RPCIII-1D
AQ282107 RPCIII-94
AQ028649 CIT-HSP-2
AA442529 zv68b02.s
AA815210 ak64h01.s
AA815141 ob48h02.s
AM083640 xc49f62.x
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A0637292 RPCI -11-4
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A0485214 RPCI -11-2
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A085808 EST99495
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AA078003 7H12D08 C
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B48914 RPCI11-4A12
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AA654562 nt75f10.s
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.

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 Description
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B17434 109 bp DNA GSS 04-JUN-1998
345K2.TVB CIT978SKA1 Homo sapiens genomic clone A-345K02, genomic
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Fax: 315 286 1810
Final: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1127 Std Error: 0.00
Seq primer: "Almin 3 fwd. Er from Amersham
High quality sequence stop: 102.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (basel, C., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wayle, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project

L Unpublished (1997)

Conteat: Wilson RK
Washington University School of Medicine

Conteat: Wilson RK
Washington University School of Medicine

A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fai: 314 286 1800

Fax: 314 280 1800
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/cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
calTech Human BAC Library A1"
1 30 c 31 g 24 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1832832 105 bp mRNA EST 13-JUL-1999 at72909.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone lMAGE:2377600 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             21813 TAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTGGAACTCCTGACCTCAGGTG 21872
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 TAGTIGAGACGGGGTITCACCATGGTGGCCAGGCTGGTCTCGAACTCCCGACCTCAGGTG 50
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                                                                                                                                                                                                                                                                                                                                             Score 93; DB 84; Length 109;
Pred. No. 0.22;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 ATCCGCCCACATCAGCCTCCCAAAGTGCTAGGATTATAGGTATGAGCCA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                /clone="A-345K02"
/clone_lib="CIT978SKA1"
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Location/Qualifiers
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Best Local Similarity 90.8%;
Matches 99; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr.
Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU, NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397630.
Contact: Wilson RK
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                          Length 105;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1140858"
/clone_lib="Stratagene hNT neuron (#937233)"
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Pred. No. 0.32;
                                                                                          Score 92.2; DB
Pred. No. 0.28;
                                                                                                                                      0; Mismatches
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56
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AQ264176/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

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Homo sapiens

Eutheria; Primates; Catarrhin; Hominidae; Wertebrata; Mammalia;

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

CE 1 (bases 1 to 109)

RS Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Simon, M. and Venter, J.C.

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

AL Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 103)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY 15733 TTTTTTTTGAGACAGAGTCTCACTCTATCACCCAGGCTGGAGTGCAGTGGACAATCTC 15792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TIGITITCTGAGACGGACTCTCACCTGTCACCCAGGCTGGAGTGCAGTGCAGTCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ535244 103 bp DNA GSS 18-MAY-1999
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 94; Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2313G15"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AQ028426.1 GI:3268648
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AQ535244
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E 1 (bases 1 to 106)
S Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berrey, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other_GSSs: CITBI-E1-2509A2.TR
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3-21
Class: BAC ends.
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrect Human BAC Library D"
30 c 34 g 17 t
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                                                                                                                                                                                                                                          AQ264176 106 bp DNA GSS 27-OCT-1998 CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2, genomic survey sequence.
AQ264176
AQ264176.1 GI:3792743
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1 TITITAGTAGAGACGAGGTITCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCG 60
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0.3%; Score 91.6; DB 105; Length 106;
Best Local Similarity 91.5%; Pred. No. 0.32;
Matches 97; Conservative 0; Mismatches 9; Indels 0;
                                                                         10912 TGATCCACCGCTTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTG 10957
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                                                                                                       61 TGATCTGCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTG 106
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/db_xref="taxon:9606"
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BASE COUNT ORIGIN

FEATURES

DEFINITION

AQ028426

RESULT

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Gaps

Gaps

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Indels

11;

Length 107;

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/cell_line="HeLa cell line; ATCC"
/lab_host="E. coli strain DH5 alpha"
/note="Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT).
From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Technology Branch
National Human Genome Research Institute/NIH
49 Corivent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
TT: 3014020201
Fax: 3014024735
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 105)
Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D.
2006 expressed-sequence tags derived from human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6217 TGGTGTGTGCCTGTAGTCCCAGCTACTCAGGAGCTGGGGCAGGAGAATCGCTTGAACCT 6276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA078003 105 bp mRNA EST 24-SEP-1999
7H12D08 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone
7H12D08, mRNA sequence.
AA078003 GI:1837477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TGGTGTGTGCCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATCACTTGAACCT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Apr 14, 1993 this sequence version replaced gi:693433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Chromosome 7 HeLa cDNA Library"
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Pred. No. 0.55;
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/db_xref="taxon:9606"
/clone="7H12D08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 7 (3), 281-292 (1997) 97228905
                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
  High quality sequence stop: 87. Location/Qualifiers
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Seq primer: -21M13 (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
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                          FEATURES
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www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                              library availability, please contact Pieter de Jong (pleter@de]ong, med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nk42bll.sl NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1016157 3' similar to contains Alu repetitive element;, mRNA sequence. AA5565533.1 GI:2337172 EST.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lb="RPCI-11"
/clone=lb="RPCI-11"
/sex="Wale"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11_Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7027 CCAGCACTTTGGGAGGCCAAAAAGGCGGATCATTTGAGGTCAGGAGTTCGAGACCAGCC 7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                               Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393355.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Pred. No. 0.46;
0; Mismatches 8; Indels 0;
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Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Arraying: Greg Lennon, Ph.D.
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Seq primer: -40ml3 fwd. ET from Amersham
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/organism="Homo sapiens"
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Best Local Similarity 92.2%;
Matches 95; Conservative
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                     Tel: 301 838 0200
Fax: 301 838 0208
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E 1 (Bases 1 to 105)

S Hillier L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashD-NCI human EST Project

Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133644.

Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
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                                                                                                                                                                                                                                                                                                                                                                                  ALB32832 105 bp mRNA EST 13-JUL-1999 at72909.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377600 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; nRNA sequence. AI832832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with Not I and cloned into the Not I and Eco RI sites of
the modified pT7T3 vector. Library constructed by Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco.
Location/Qualifiers
                                                                                                                                                                                                       9874 TACAAAAATTAGCCGGGCATGGTGGTGCACGCCTGTAATCCCAGCTACTTGGGAGGCTGA 9933
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                                                                                                                                 Score 89; DB 28; Length 105;
Pred. No. 0.62;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                            /clone="IMAGE:2377600"
/clone_lib="Barstead colon HPLRB7"
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/db_xref="taxon:9606"
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                                                                                                                                 ch 0.3%;
1 Similarity 90.5%;
95; Conservative (
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Fax: 314 286 1810
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Length 105;

DB 61;

Score 89;

0.3%;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 103)
S Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@delong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                     AAGCTGAGACAGGAGAATCGCTTGAACCTGGGAGGCGGAGGTTGTGGTGAGCCGAGATCA 20788
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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                                                                                                              105 AGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGGTTGCGGTGAGCCCAAGATCG 46
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  Indels
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                                                                                                                                                                                                 45 CACCATTGCACTCCAGCCTGGGCAACAAGAGCGAAACTCTGTCTC 1
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10;
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91.3%; Pred. No. 0.69;
tive 0; Mismatches
Mismatches
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1. 103
/organism="Homo sapiens"
/db_xref="GDB:7501163"
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/clone="RPCI-11-4A12"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                       103 bp
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Admas, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Unpublished (1998)
Unpublished (1998)
Unpublished (1998)
Unpublished (1998)
Unpublished (1998)
Universely and Mans Department of Eukaryotic Genomics
The Institute for Genomic Research
Fre Institute for Genomic Research
Frax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@tesgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 102)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3 Reverse
Class: BAC ends.
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/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBeloBAC11; Site_1: EcoRI;
/note="Vector: pBeloBAC11; Site_1: EcoRI;
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Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
912 Medical Center Dr., Rockville, MD 20850, USA
791: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.3%; Score 88.2; DB 105; Best Local Similarity 88.1%; Pred. No. 0.74; Matches 96; Conservative 0; Mismatches 13; 1
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/db_xref="taxon:9606"
/clone="2510E2"
/clone_lib="CITBI-E1"
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1. .109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pieter de Jong pieter/dealong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:

**Research Genet cs (info@resgen.com). BAC end search page:

Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)
2hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
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/sex="Male"
/cell_type='Lymphocytes"
/note='Vector: pBAC63.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbeetigr org
Clones are derived from the human BAC library RPCI-11. For BAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                   18-MAY-1999
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Pred. No. 0.69;
0; Mismatches 9; Indels 0;
                                                           AQ535244 103 bp DNA GSS 18
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
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/organism="Homo sapiens"
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AQ265749.1 GI:3791503
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AQ535244.1 GI:4846934
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Best Local Similarity 91.3%;
Matches 94; Conservative (
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RESULT
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/lab\_host="DH10B"

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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index

Tumor Gene Index

On Jan 19, 1998 this sequence version replaced gi:2151346.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA807640 103 bp mRNA EST 05-MAR-1998 nx08b05.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255473 3' similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5386 GCCCAGGCTGGAGTGCAATGGCGGGATCTCGGCTCACCGCAACCTCTACCTCCCAGGTTC 5445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 103)
                                                                                                                                                                                                                                                                                                                      /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87.6; DB 94; Length 102;
Pred. No. 0.89;
0; Mismatches 9; Indels 0
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/db_xref="taxon:9606"
/clone="lmAGE:1255473"
/clone_lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5446 AAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTAC 5487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AAGCGACTCTCCTGCCTTAGGCTCCCGAGTAGCTGGCATTAC 102
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Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 87.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                          /db_xref="GDB:7151269"
/db_xref="taxon:9606"
/clone="2292A10"
/clone="11b="CIT-HSP"
/sex="Male"
                                                                                                                           Location/Qualifiers
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AA807640.1 GI:2877108
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91.2%;
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Best Local Similarity
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AA807640
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KEYWORDS
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                  10857 ATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC 10916
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                           Length 103;
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Pred. No. 0.88;
0; Mismatches 9;
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Job time: 317638 sec
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Best Local Similarity 91.2%;
Matches 93; Conservative (
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                                                                                                                                                                         BASE COUNT
ORIGIN
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Sequence:

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Searched:

Database

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SOFTWARE: PACENTIN RELABES #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: PC-1003/MS-1005
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICAȚION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: LAUGET, LEONA L.
REGISTRATION NUMBER: 30,863
REFERENCE,/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1905
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US-08-340-426D-70
US-08-450-673C-70
PCT-US55-17111A-70
US-08-340-426D-69
US-08-450-673C-69
US-08-450-673C-69
US-08-454-557C-57
US-08-450-673C-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-084.481-658B-65/c
Sequence 65, Application US/08481658B
Sequence 55, Application US/08481658B
Sequence 55, Application US/08481658B
SEMERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastcrek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NO
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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     COMPUTER READABLE FORM:
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California
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US-08-481-658B-65
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  STATE:
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10130.869 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6C_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/6COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PorruS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/Packfiles1.seq:*
                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-454-557C-70
US-08-340-426D-70
US-08-450-673C-70
PCT-US95-17111A-70
US-08-454-557C-70
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US-08-485-862B-65
US-08-7139-65
US-08-477-504A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-485-862B-65
US-08-485-862B-65
US-08-45-65-91
US-08-45-670-91
US-08-450-673C-91
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US-08-340-426D-91
US-08-450-673C-91
PCT-US95-17111A-91
US-08-454-557C-92
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US-08-450-673C-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230463 seqs, 64992525 residues
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Listing first 45 summaries
                                                                                                                                     - nucleic search, using sw model
                                                                                                                                                                                        June 18, 2000, 01:37:37
                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Query
Match Length D
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Maximum DB seq length: 110
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US-08-486-756A-65/c
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                                      6099 ATCCCAGCACTTTGGGAGGTCGAGGCAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6099 ATCCCAGCACTTTGGGAGGTCGAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGAGTTTGAGAGCAGC 46
  0; Gaps
                                                                            105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTONNEY-AGENT UNCHMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 105;
0; Mismatches 15; Indels
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Pred. No. 8.6e-10;
0; Mismatches 15; Indels
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                                                                                                                       6159 CTGACCAAAATGATGAAACCCTGTCTTCTACTAAAAATACAAACA 6202
                                                                                                                                          45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
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Sequence 65, Application US/08477504A

Patent No. 5972353

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.3
Best Local Similarity 85.6
Matches 89; Conservative
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-477-504A-65
Matches
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6099 AICCCAGCACTTTGGGAGGTCGAGGCAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PETENTIN STATEM.
SOFTWARE: PETENTIN BATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY, AGENT INFORMATION:
NAME: LAUGHT, LEONA L.
REGISTRATION NUMBER: 30,863
REFERENCE/POCKET UNDRER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 105;
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Best Local Similarity 85.6%; Pred. No. 8.6e-
Matches 89; Conservative · 0; Mismatches
; Sequence 65, Application US/08486756A

; Patent No. 5981711

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Application US/08485862B
Fatent No. 5999838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 15-435-0727
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                      CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-485-862B-65/c
                                                                                                                                                                                                                                                                                                                                         94920
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US-08-486-756A-65
                                                                                                                                                                                                                                                                                                                  COUNTRY:
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RESULT

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6099 ATCCCAGCACTTTGGGAGGTCGAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 80; DB 5; Length 105;
35.6%; Pred. No. 8.6e-10;
Lve 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6159 CTGACCAAAATGATGAAACCCTGTCTCTACTAAAAATACAAACA 6202
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Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ITLLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STREET: 6 Mariposa Court
CITY: Tiburon
STREET: 6 Alfornia
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
                   FILING DATE: 24-JAN-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: O7-JUN-1995
FILING DATE: O7-JUN-1995
                                                                                                                                                                                                                                                                                                                          PRIOR DATE: 0/10/11393
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/485,862
FILING DATE: 0/10/1195
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/485,863
FILING DATE: 0/10/1195
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/487,077
FILING DATE: 0/10/1195
ATTORNEY/AGENT INFORMATION: NAMME: LAUGEY, LEONA L. NAMME: LAUGEY, LEONA L. REGISTRATION NUMBER: 30,863
JMBER: US/08/787,739
24-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.3%;
Best Local Similarity 85.6%;
Matches 89; Conservative
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TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-481-658B-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-08-787-739-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: OPPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/477,504
FILING DATE: 15-JUN-1994
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
APPLICATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REFERENCE/POCKET NUMBER: D-0021.3D
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 105;
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Best Local Similarity 85.6%; Pred. No. 8.6e-10;
Matches 89; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-787-739-65/c

Sequence 65, Application US/08787739

Patent No. 6027887

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                        California
Tiburon
                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO US-08-485-8628-65
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                                                                    ZIP: 94920
                      STATE: COUNTRY:
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Lauder, Leona L.
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CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94920
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                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE:
US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-486-756A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.3%; Score 79.4; DB 4; Length 105; Best Local Similarity 84.8%; Pred. No. 1.2e-09; Matches 89; Conservative 0; Mismatches 16; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRICA PLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QY 10903 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN.1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTGACCTTGTGATCCACCAGCCTCCGCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ATILE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    D-0021.3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-504A-65; Sequence 65, Application US/08477504A; Patent No. 5972353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTX: USA
ZIP: 94920
                                                                                                                                                                                                                                                                          NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEO ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-08-481-658B-65
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QY 10843 TITITIGIATITITATITAGAGAIGGGGTTTCACCAIGTIAGCCAGGAIGGICTCGAICTC 10902
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0.3%; Score 79.4; DB 4; Length 105;
Best Local Similarity 84.8%; Pred. No. 1.2e-09;
Matches 89; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR PATICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY APPLICATION NUMBER: US 08/260,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY 10903 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10947
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; Patent No. 5981711
; GENERAL INFORMATION:
    APPLICANT: Zavada, Jan
    APPLICANT: Pastorekova, Silvia
    APPLICANT: Pastorek, Jaromir
    TILLE OF INVENTION: MN Gene and Protein
    NUMBER OF SEQUENCES: 86
    CORRESPONDENCE ADDRESS:
                                D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-0021.3C
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0234
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 DIMENSON TOPOLOGY: Linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDRESSEE: Leona ...
                                                                                                                                                                                 LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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10843 TTTTTTGTATTTTTATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 10902
                                          1 TITITIACATCITIAGAGACAGGGITICACCATATIGGCCAGGCIGCTCTCAAACIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: F10PPy disk
COMPUTER: I USA
COMPUTER: F10PPy disk
F11ING DATE: C10PN-1995
F11ING DATE: O7-UNN-1995
F11ING DATE: O7-UNN-199
                                                                                                                               OY 10903 CIGACCICGIGATCCACCCCCTTTGGCCTCCCAAAGTGCTGGGAT 10947
                                                                                                                                                                61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                     ; Sequence 65, Application US/08783739
; Patent No. 6027887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
R: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO
US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                      RESULT 10
US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                 g
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                                                                                                                                                                                                                                                                                                                    Qy 10843 TTTTTGTATTTTATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 10902
                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                        1 TITITACATCTTTAGTAGAGACAGGGTTCACCATATTGGCCAGGCTGCTCTCAAACTC 60
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84.8%; Pred. No. 1.2e-09;
tive 0; Mismatches 16; Indels
                                                                                                                                                                                       0.3%; Score 79.4; DB 4; Length 105;
84.8%; Pred. No. 1.2e-09;
tive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 10903 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 65, Application US/08485862B
Patent No. 598938
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
WUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-0021.3D
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REGISTRATION NUMBER: 30,863
REFRENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0334
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO; ANTI-SENSE: NO US-08-486-7568-65
                                                                                                                                                                                    Query Match 0.3%
Best Local Similarity 84.8%
Matches 89; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.3
Best Local Similarity 84.8
Matches 89; Conservative
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COMPUTER READABLE FORM:
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US-08-485-862B-65
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GENERAL INFORMATION:
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Alzheimer's Disease
UNUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                  10843 TTTTTTGTATTTTATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 10902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10875 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCCGCTTTGGCCTCCC 10934
                                                                     Gaps
                                                                                                                                              Gaps
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                 0.3%; Score 79.4; DB 5; Length 105;
84.8%; Pred. No. 1.2e-09;
tive 0; Mismatches 16; Indels
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86.7%; Pred. No. 2e-06;
tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                            QY 10903 CTGACCTCGTGATCCACCGGTTTGGCCTCCCAAAGTGCTGGGAT 10947
                                                                                                                                                                                                                                        61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005-3934

ZIP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MXY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwidy, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
TELECPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELEFRAXION FOR SEO ID NO: 91:
FROMMATION FOR SEO ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                            Sequence 91, Application US/08454557C Patent No. 5830670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 91, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oy 10935 AAAGTGCTGGGATTACAGGCGTG 10957
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Best Local Similarity 86.7<sup>3</sup>
Matches 72; Conservative
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LENGTH: 84 base pairs
                                          Best Local Similarity 84.8
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Wash
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-454-557C-91
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US-08-340-426D-91
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                      Query Match
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Sequence 91, Application US/08450673C
Sequence 91, Application US/08450673C
Patent No. 5948888
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                 Protein Gene Expression and Detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10875 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCCGCTTTGGCCTCCC 10934
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Pred. No. 2e-06;
0; Mismatches 11; Indels
                                                                                                                                                                                          ALLICATION OF A VOID STATE: D.C. STATE: D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein G
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.2%;
Best Local Similarity 86.7%;
Matches 72; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20005-3934
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TOPOLOGY:
US-08-340-426D-91
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Length 84;

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Qy 10875 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCCGCTTTGGCCTCCC 10934
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LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
Matches 70; Conserv
  ; TOPOLOGY: both PCT-US95-17111A-91
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US-08-454-557C-91/c
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GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 65.4; DB 4; Length 84;
86.7%; Pred. No. 2e-06;
tive 0; Mismatches 11; Indels
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                                                                                        ATTUNNUL/ANGERA ANGERIA ANGERIA MAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION:
               APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity 86.79
Matches 72; Conservative
CURRENT APPLICATION DATA:
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PCT-US95-17111A-91
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US-08-450-673C-91
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                                                                 APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 0609.3840003
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
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illarity 85.4%; Pred. No. 7.9e-06;
Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 91, Application US/08454557C; Patent No. 5830670; GENERAL INFORMATION:
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Search completed: June 18, 2000, 09:57:10 Job time: 334960 sec

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         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 110
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Perfect score:
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50: gb\_pt3:\*
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9		HSLDLRN2	HSLDLRN2	HUMALCE162	HSU67803	HUMALCE221	HUMALCE221	HUMALCE272		HSLDLRD2					HSU67803	HUMALCE43	HUMALCE272	HSU67808	HSU67808	HUMALCE43	HUMALCE162	G32743	HSU67804	HS81C8R	HS8IC8R	Ξ		HSU67806	HSU67804		HSU67806	HUMULUUSMS	HSU6/80/	HUMLDLRA2	HUMGALNSA	HUMBRKFAE	HUMUT8002B	_	879560	HUMD1D03M5	AR051521	HUMLDLRFL	632906	HUMUT931A	HSLAS27
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KEYWORDS
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AUTHORS
TITLE
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SOURCE
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ORIGIN
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                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
Bur. J. Biochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotta; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (Dases 1 to 108)

Horsteneke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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                                                   20-MAY-1992
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                                                                                                     X05250.1 GI:34337
Alu repetitive sequence; low density lipoprotein receptor
                                              HSLDLRN2 108 bp DNA PRI 20-MAY.
Human LDL-receptor gene intron 14 fragment (normal gene)
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
LOCATION/Qualifiers
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 92; DB 10;
90.7%; Pred. No. 2.2e-06;
11ve 0; Mismatches 10
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23 c 39 g 18 t
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Matches 98; Conservative
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MEDLINE
            RESULT
HSLDLRN2
                                                                                   ACCESSION
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KEYWORDS
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Homo sapiens
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Butharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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1 (bases I to 108)
Shaikh, T. H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                             HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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                                                                                                                                                                               Length 108;
                                               10; Indels
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  Score 92; DB 10;
Pred. No. 2.2e-06;
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Human small cytoplasmic Alu transcript.
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                                          0; Mismatches
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30 c 35 g 1
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/sex="male"
0.38;
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                                            98; Conservative
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  Query Match
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source

FEATURES

TITLE JOURNAL

AUTHORS

MEDLINE REFERENCE BASE COUNT

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Alu repeat.

Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens

Bulkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences

J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24288 CTGGAGTGCTGTGGCACGTTCTCGGCTCACTGCAACCTCCGCCTCACGGGTTCAAGCGAT 24347
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1 (bases 1 to 104)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 CTGGAGTGCAATGGCACGATCTCGGCTCACTGCAACCTCCCGCCTCCCGGGTTCAAGCGAT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMALCE272 104 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE272.
M87899
                                                     HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87895 GI:174874
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Homo sapiens male embryo carcinoma cDNA to other RNA
Homo sapiens
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Pred. No. 5.7e-05;
0; Mismatches 12; Indels
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90.8%; Pred. No. 6.1e-05;
tive 0; Mismatches 9;
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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26 c 37 q 1
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/db_xref="taxon:9606"
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/dev_stage="embryo"
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Best Local Similarity 88.3
Matches 91; Conservative
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               2 (bases 1 to 108)
Shaikh, T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (12-40G-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Clvic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Homo sapiens
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Pred. No. 5.2e-05;
0; Mismatches 10; Indels
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Pred. No. 1.1e-05;
0; Mismatches 5
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27 c 33 g 18
                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                           /clone="TscAlu2"
                                                                                                                                                                                                                               1. .108
/note="scAlu"
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94.8%;
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Best Local Similarity 94.88
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Best Local Similarity 90.v.
Best Local Similarity 90.v.
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97415756
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DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

HUMALCE221

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JOURNAL

FEATURES

BASE COUNT

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Williamson, R. and Humphries, S.
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1 (bases 1 to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-veer between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
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                                                                                                                                                                                                                                   20-MAY-1992 deletion junction.
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                  17750 CCATGTTGGTCAGGCTGGTCTTAAACTCCTGACCTCATGATCTGCCCACCTCAGGCTCCT 17809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="deletion junction region intron 12/ intron 15" 40 c 20 q 28 t
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                                                    104 CCATGTTAGCCAGGCTGGTCTTGAACTCCTGGCCTCGCAATCTTCCCTCCTCAGCCTCCC 45
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
                                                                                                                                                                                                                                                                                                              Alu repetitive sequence; low density lipoprotein receptor
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Pred. No. 7.7e-05;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GTAGCTGGGATTACAGGCACCTGCCACCCCGCCTGGCTAATTTTGT 108
                                                                                             17810 AAAGTGCTGGGATTACAGGCGTGAGCCACCCCCCCCCCGGCCAGA 17852
                                                                                                                                                                                                                     HSLDLRD1 108 bp DNA PRI
Human LDL-receptor mutated gene with intron 12
X05249
                                                                                                                 AAAGTGCTGGGATTACAGGAGTGAGCCACCGGGCCGGCCAGA 2
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Best Local Similarity 86.0%;
Matches 92; Conservative
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*source: hypercholesterol aemia
see X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
allu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNN.
Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 12 deletion junction.
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
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Pred. No. 7.7e-05;
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Bukaryota: Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 108)

1 (Abases I to 108)

1 (Abases I to 108)

Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for Eur. 3 Biochem. 164 (1), 77-81 (1987)
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
density lipoprotein.
                                                                                                                                                                                       Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91)
Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L.,
Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X.,
Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4077 TCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACCATTGCACTCCAGCCTGGGTGACA 4136
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91.2%; Pred. No. 0.00052;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Denaturation: 94C 300sec
                                                                                                                                                                                                                                                                                                                                  Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
primer A: AGAGGTTGCAGTGAACCAA
Primer B: TTTTTCCCCTCTTACTCACT
End to Label: Primer B
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20 c 23 g
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HSLDLI12/c
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KEYWORDS
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1 (Bases I to 108)

1 (Bases I to 108)

1 (Bases I to 108)

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
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                                                                                                                 Qy 10935 ACAAAAGTTAGCTGGGCGTGGTGGCACATGCCTGTAGTCCCAGCTACTGGGGAGGCTGAG 10994
                                                                          Gaps
                                                                                                                                             108 ACAAAAATTAGCCAGGCGGGGGGGGGGGGGCGGGTAATCCCAGCTACTCGGGAGGCTGAG 49
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85.0%; Pred. No. 0.00015;
iive 0; Mismatches 16; Indels 0
                           Length 108;
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
                      Score 81.4; DB 10;
Pred. No. 0.00015;
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/db_xref="taxon:9606"
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ilarity 85.0%;
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Matches 91; Conserv
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                        Query Match
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JOURNAL MEDLINE COMMENT

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See X05249 for deletion junction Data kindly reviewed (07-DEC-1987) by HUMPHRIES S. Location/Qualifiers

87161901

JOURNAL MEDLINE

FEATURES

COMMENT

L30244.1 GI:605447 STS; PCR primer; STS sequence; microsatellite DNA; microsatellite ansker; sequence tagged site; tetranucleotide repeat. Homo sapiens DNA.

DEFINITION

ACCESSION VERSION KEYWORDS

SOURCE

HUMUT8164A

RESULT 12

BASE COUNT

ORIGIN

FEATURES

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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

DEFINITION

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RESULT 11

HSLDLRD2

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Search completed: June 18, 2000, 17:40:24 Job time: 363708 sec
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Live 0; Mismatches 12; Indels 0;
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0; Mismatches 16;
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Human small cytoplasmic Alu transcript.
U67803
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/note="intron XII fragment"
/note="intron XII fragment"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
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/db_xref="taxon:9606"
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/rpt_type=dispersed
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Matches 88; Conservative
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Matches 85; Conservative
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                                                                                                                      Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens
Homo sapiens
Homo sapiens
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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HUMALCE43 110 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE43.
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/db_xref="taxon:9606"
/dcell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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A single-stranded DNA, Or its complementary strand or the corresp.

double-stranded DNA, which comprises one of the 7837 "GS" sequences
given in T19001-T25837 and which is able to hybridise to part of
human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNAs pecies, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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Human gene signature HUMGS06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 95-206931/27.

Identifying gene signatures in 3'-directed human cDNA library - e.g., for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
           gene
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T24892 standard; cDNA to mRNA; 100 BP.
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Best Local Similarity 81.6
Matches 80; Conservative
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12-NOV-1993; JP-355504.
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Match Length
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Maximum DB seq length: 110
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57.
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665.8
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663.6
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                     A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 GS* sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Beach library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 2 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease claim 1; Page 219; 310pp; English.
                                    Human gene signature HUMGS06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CCTGGGTGACAGAGTGACACTCTGTTTGAAACAAA 100
                                                                                            cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1998.
05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                   05-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2
Best Local Similarity 80.8
Matches 80; Conservative
                                                                                                                                                             01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                  Okubo K;
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Homo sapiens.
WO9820165-A2.
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WPI, 95-206931/27.
                                                                                                                                         W09514772-A1.
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markers which have been isolated using the primers represented in markers which have been isolated using the primers represented in (X09121-X10268. The beam isolated using the primers represented in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases cuch as agammaglobulinemia, diabetes insiplidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercytosis, von Willebrand's disease, hereditary cancertolesterolemia, polycystic kidney disease, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Bhlers-Danlos spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Bhlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoinmunne diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed autoince, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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A single-stranded DNA which comprises one of the 7837 "GS" sequences couble-stranded DNA, which comprises one of the 7837 "GS" sequences and missing the complementary strand couple of part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared to manna risussing poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost intranslated sequence is unique to a particular mRNA species, almost is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7549 CTGTAATCCCAGCAC-TTTGGGAGGCTGAGGTGGATCACCTGAGGTTGGGAGTTTG 7607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 CTATAATCCCAGCACTTTTGGGAGGCCAAGGCAGACGGATCACTTGAAGTCAGGAGTTCG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1996 (first entry)
Human gene signature HUMGS09078.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66.8; DB 1; Length 108;
Pred. No. 0.055;
1; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7608 AGACCAGCCTGGCCAACATGGTAAAACCCCATGTCTACTAAAAATACA 7655
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T26828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prophylaxis of such diseases.
Sequence 108 BP; 19 A;
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Matches 88; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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(OKUB/) OKUBO K.
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double-stranded DNA, or its complementary strand or the corresp.

double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 91 BP; 18 A; 22 C; 28 G; 18 T;
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WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
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Human gene signature HUMGS09078.

Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell fryping; abnormal cell function; ss. W09514772-A1.
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Pred. No. 0.13;
...matches 17; Indels
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0; Mismatches
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                                                  멾.
                                               T25854 standard; cDNA to mRNA; 91
                                                                                        22-OCT-1996 (first entry)
Human gene signature HUMGS08084.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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11-NOV-1994; J01916.
12-NOV-1993; JP-35564.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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WO9514772-A1.
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    RESULT
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Claim 1: Page 219; 310pp; English.

Claim 1: Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, mascular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary syndrome, osteogenesis inmerfected, acute internitent porphyria, autolimmune diseases, inflammation, cancer, diseases of the nervous syndrome, osteogenesis inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longerity, appearance (e.g. baldness, obseitly), strength, speed, canturance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid converted and the converted medicaments for the treatment or prophyriane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human biallelic polymorphic DNA fragment TIGR-A003M18a. Polymorphism, biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                  Gaps
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                                                                  Length 108;
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  28
                                                  Score 65.2; DB 1; Pred. No. 0.094;
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  23
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06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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33
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108 BP; 19 A;
                                                                  0.2%;
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86; Conservative
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  18
                                                                                                              76; Conservative
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  BP;
                                                                                          Best Local Similarity
108
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WO9820165-A2.
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  Sequence
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Matches

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a

23 T;

25 G;

21 C;

33 A;

103 BP;

Sednence

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                                                                 A single-stranded DNA) which complementary strand or the corresp.

A single-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA was intriated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-en of or mRNA by using poly(T) as particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed as oa st or reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for seconising different cell types.

Sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11604 GATCTCCTGACCTCGTGATCGGCCCCCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGT 11663
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Human gene signature HUMGSO8452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                        0.2%; Score 64.4; DB 1; Length 108; 80.4%; Pred. No. 0.12; ive 0; Mismatches 18; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 11664 GAGCCACTGCGCCCGGCCCCGTTTTTTTTT 11695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GAGCCACCACGCCGGCTGTTTTATTCTTAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell typing; abnormal cell function; ss. W09514772-Al.
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                                                     Claim 1; Page 2182; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T26213 standard; cDNA to mRNA; 103
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.29
Best Local Similarity 80.4
Matches 74; Conservative
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11-NOV-1994; JO1916.
12-NOV-1993; JP-355504.
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WPI, 95-206931/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lissue 1: Page 758-759; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                        Gaps
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                                                                                                                                                                 1 GATCACTTGAGTCCAGGAGTTTGGTGTTACAGTGAGCTATGATGGCACCACTGCACTCCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1996 (first entry)

Human gene signature HDMGS02180.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abnormance of corresp. mRNA in specific human
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  Length 103;
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                                                     Indels
                                                                                                                                                                                                                          QY 10160 GCCTGGGCAACAATGCAAAATCCTGTCTCAAAAACAAAACA 10201
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76.0%; Pred. No. 0.21;
tive 0; Mismatches
                                                     0; Mismatches
Score 63.6;
Pred. No. 0.
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0.2%;
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB/) OKUBO K.
                                                     78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Query Match
Best Local Similarity
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Matches 76; Conser
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                                                        Matches
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ID T209
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T20927
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Claim 1; Page 1944; 2245pp; Japanese
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA, which comprises one of the 7817 "63" sequences of given in T19001-T25837 and which is able to hybridise to part of caylen in T19001-T25837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end than a sole primer is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs. In the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                       Human gene signature HUMG502180.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
Homo sapiens.
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cell typing; abnormal cell function; ss.
Homo sapiens.
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ID T25854 standard; cDNA to mRNA; 91
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22-0CT-1996 (first entry)
Human gene signature HOMGS08084.
             4-JUL-1996 (first entry)
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Best Local Similarity 76.59
Matches 75; Conservative
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K. Okubo K;
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                    Matsubara K, Okubo K;
WPI; 95-206931/27.
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A single-stranded DNA, which complementary strand or the corresp.

C abling in 19901-72683 and which comprises one of the 7837 "GS" sequences glove in 19001-72683 and which comprises one of the 7837 "GS" sequences glove in 19001-72683 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNA hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (asp. using primers and probes derived from the GS crossonising different cell types.
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Human gene signature HUMGS08452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
WO9514772-A1.
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Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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0; Mismatches
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Best Local Similarity 78.7%;
Matches 70; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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Human biallellc polymorphic DNA fragment EST98276a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autolimnue disease; cancer; inflammation; drug; medicament;
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        DB 1; Length 103;
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                                                                                                                                                                                                                                                                      42 TCATAGCTCACTGTAACACCCAAACTCCTGGACTCAAGTGAT 2
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                                   Pred. No. 0.39;
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           Score 61;
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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ID x12085 standard; DNA; 100 BP.
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Best Local Similarity
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WO9820165-A2.
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While year Accoptory 22.

New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity resting or phenotypic typing for disease

Claim 1; Page 218; 310pp; English.

Claim 1; Page 218; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammagolobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary capteroxis, von Willebrand's disease, tuberous sclerosis, phere-Danies are propertied interinitent porphyria, appearance (e.g. baldness, obesity), strength, speed, autolimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid areas manner or expensively.
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                              Human biallelic polymorphic DNA fragment EST98276c.
Polymorphism, biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276b.
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Pred. No. 0.63;
1; Mismatches 25;
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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05-NOV-1997, U20313.
06-NOV-1996, US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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(first entry)
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WO9820165-A2.
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PT determining polymorphic forms for use in e.g. forensics, paternity PT determining polymorphic typing for disease
Claim 1; Page 219; 310pp; English.

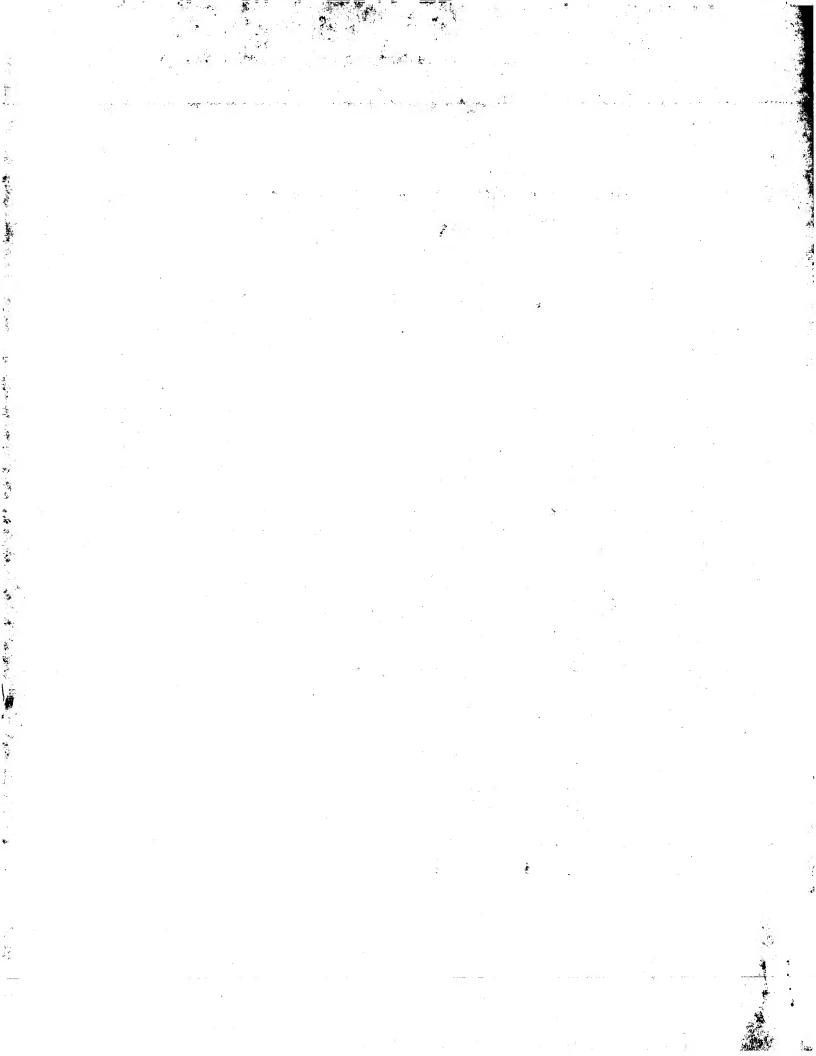
X10269-X12937 are human DNA fragments which contain biallelic polymorphic X10269-X12937 are human DNA fragments which contain biallelic polymorphic of an arkers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes instpidus, Lesch-Nyhan syndrome, c.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes instpidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous solerosis, hereditary spherocytosis, now Willebrand's diseases, tuberous solerosis, papearand and subsceptibility cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid copposity solenoes also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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ö 0; Gaps Query Match 0.2%; Score 59.6; DB 1; Length 100; Best Local Similarity 74.0%; Pred. No. 0.63; Matches 74; Conservative 1; Mismatches 25; Indels

4856 TGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCATCTGAGG 4915 100 TGTGACTCACCACCTATAATCCTGGCACTTTAGGAGGCTKAGGAAGAAGAGGATGTTTGAAA 41 õ g

4916 TCAGAAGTTCCAGACCAGCCTGGCCAACATGGCGAAACCC 4955 40 CCAGGAGCTCAAGACCATCCTGGGAAACATAGCAAGACTC 1 ò

Search completed: June 18, 2000, 18:17:42 Job time: 364773 sec



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9D est1: **
9D est2: **
9D est5: **
9D est6: **
9D est6: **
9D est1: **
9D est11: **
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em_est11:*
em_est13:*
em_est13:*
em_est14:*
em_est15:*
em_est15:*
em_est17:*
em_est17:*
em_est17:*
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em_est4:*
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em_est6:*
em_est7:*
em_est8:*
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Maximum DB seq length: 110
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Perfect score:
                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                  Searched:
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Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 102.
 Contact: Wilson RK
                                                                                                                                                                                                                                  99; Conservative
                                                                                    1. .106
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                    Query Match
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                                                                                     source
                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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                                                                            FEATURES
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AQ282340 RPCI11-80
AQ54957 CITBI-E1-
AQ33497 wm74d02.x
AQ028426 CIT-HSP-2
                                                                                                                                                                                                  A1991750 wt48e01.x
A1991750 wt48e01.x
AA385808 EXT9945
AA583697 nn58f10.s
AA7870764 ac68f12.s
AA21888 ZG1504.s
AA385808 EGT99495
                     AA243009 zr25h02.s
B17434 345K2.TVB C
A1077628 0y26f04.s
AA835205 ak64h01.s
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A0386882 RPCI11-13
                                                                                                                                                                     AQ028649 CIT-HSP-2
AQ535244 RPCI-11-3
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AQ240182 CIT-HSP-2
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AA078003 7H12D08 C
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                                                                                           AQ264176 CITBI-E1-
                                                                                                                                                                                                                                                        AQ582186 RPCI-11-4
AQ582186 RPCI-11-4
                                                                                                   14245 nc07a04.s
                                                                                                                        AA897366 am06h02.s
                                                                                                                                                                                            AA243009 zr25h02.s
                                                                                                                                                                                                                                                                               AA565533 nk42b11.s
                                                                                                                                                                                                                                                                                                                                                                                                                     AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:11140858 5' similar to contains Alu repetitive element;, mRNA
                                                     B48914 RPCI11-4A12
B17434 345K2.TVB C
                                                                    AQ028426 CIT-HSP-2
AQ003188 RPCI11-1D
                                                                                                          H67040 yu68c01.rl
B65160 CIT-HSP-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Frimates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.

Washl.NCI human EST Project
 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397630.
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                              AA565533
AQ634950
AA583697
AA078003
AQ534922
AQ500347
                                                                                                                        AA812141
AA897366
AA565533
AQ240182
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AQ582186
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AQ282340
AQ544957
AI933497
AQ028426
                                                         B17434
AQ028426
AQ003188
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A1991750
A1991750
AA385808
AA583697
AA780764
AA218889
                                     AI077628
AA835205
                                                                                   AQ386882
                                                                                                                                                        AA807640
                                                     B48914
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                                                                                                                                               103
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Length
Match
              naman.
              VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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/organism="Homo sapiens"
/db_xref="Haxon:9606"
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/clone="IMAGE:1140868"
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Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-Zap XR Vector; -5' adaptor sequence: 5'
GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT" 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zr25h02.sl Stratagene NT2 neuronal precursor 937230 Homo sapiens 2DNA clone IMAGE:664467 3' similar to contains Alu repetitive element; contains element LTR1 repetitive element; , mRNA sequence. AA243009.1 GI:1873869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11559 TITITAGIAGATACGGGGTTTCACTTTGTTAACCAGGATGGTCTCGATCTCCTGACCTCG 11618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 109)
Hillar, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washd-NCI human EST Project
Unpublished (1997)
On Dec 3, 1996 this sequence version replaced gi:1126869.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 Er from Amersham
High quality sequence stop: 53.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1127 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TITITAGTAGAGGACGAGGTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94.8; DB 37; Length 106; Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy 11619 TGATCGGCCCCCCCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTG 11664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.3%; Score ... 93.4%; Pred. No. 0.04; ... 0; Mismatches
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National cancer
Tumor Gene Index
I Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2153443.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 820 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Incation/Qualifiers
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                                                                                                                                                                                                                 Qy 19510 TAGTAGAGATGGGGTTTCACCATGCTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGCG 19569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 100)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pT/T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1077628 100 bp mRNA EST 24-SEP-1998 oy26f04.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1666975 3' similar to gb:x57130_cds1 HISTONE HID
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                     109 TAGTIGAGACGGGGTTTCACCATGGTGGCCAGGCTGGTCTCGAACTCCCGACCTCAGGTG 50
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/clone=!hmdE:1666975"
/clone=lib="Soares senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="bH10B (ampicillin resistant)"
                                                                                                                                                   ö
                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                             Qy 19570 ATCTGCCCGCCTCAGCCTCCCAAAGTGCTAGGATTACAGGCGTGAGCCA 19618
                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 0.2;
0; Mismatches 7;
                                                                                    Score 91.4; DB 84;
Pred. No. 0.098;
                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMAN);, mRNA sequence.
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Best Local Similarity 93.0%;
Matches 93; Conservative (
                                                                                        0.3%;
                                                                                                                        Best Local Similarity 89.9
Matches 98; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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TITLE
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KEYWORDS
SOURCE
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/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library A1"
1 30 c 24 t
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Nealey, J. M., Rounsley, S. R. and Venter, J. C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1997)
Other_GSSs: 345K02.TP 345K02.TPB
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B17434 109 bp DNA GSS 04-JUN-1998
345K2.TVB CIT978SKA1 Homo sapiens genomic clone A-345K02, genomic
survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.ilgr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oy 11556 GTATTTTAGTAGATACGGGGTTTCACTTTGTTAACCAGGATGGTCTCGATCTCCTGACC 11615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTATTTTTAGTAGAGAGGGGTTTCACCGTGTTAGCCAGGATGGTCTTGATCTCCCTACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy 11616 TCGTGATCGCCCCCCCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTG 11664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCGTGATCCGCCCACCTCCGGCCTCCCAAAGTGCTGGGATTACAGGCGTG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91.4; DB 30;
Pred. No. 0.098;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. . 109
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/clone="A-345KO2"
/clone="CIT978SKA1"
                                                          /organism="Homo sapiens"
                                                                                    /db_xref="GDB:5426481"
                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B17434.1 GI:2125183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.39
Best Local Similarity 89.99
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: T7
Class: BAC ends.
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                                source
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ORGANISM
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AUTHORS
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JOURNAL
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B17434/C
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KEYWORDS
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FEATURES
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us-08-852-495c-2\_copy\_56000\_85000.rst

LOCUS

AA835205

RESULT

g ŏ g ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

08-APR-1999

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Adams M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadamsétigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
thtp://www.tigr.org/tdb/humgen/bac_end_search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA GSS 04-JUN-1998
Homo sapiens genomic clone A-345K02, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 11555 TGTATTTTAGTAGATACGGGGTTTCACTTTGTTAACCAGGATGGTCTCGATCTCCTGAC 11614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="mare"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
28 c 30 g 15 t
                                           RPCIII-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12,
                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 84; Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88.6; DB Pred. No. 0.21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cocation/Qualifiers
1. 103
/organism="Homo_sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GDB:7501163"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RPCI-11-4A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11"
/sex="Male"
                                                                     genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%;
Best Local Similarity 91.3%;
Matches 94; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B17434 109 bp
345K2.TVB CIT978SKA1
                         103 bp
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                                                                                                                B48914.1 GI:2601151
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                                                                                                                                                            human.
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DEFINITION
                                           DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
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VERSION
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                                                                                                                VERSION
KEYWORDS
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SOURCE
    B48914/c
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B17434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                               AA835205 101 bp mRNA EST 23-FEB-1998 ak64h01.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412689 3' similar to contains Alu repetitive element; contains element KER repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theisling,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy 11402 GAGACGGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGTGTGTCTCCGCTCACTG 11461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100 AAGAGCCTGTGGAGCAAGGCGACTCTAGTGCAAACGAAAGGCACCGGTGCTTCTGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On Nov 29, 1993 this sequence version replaced g1:636191.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Barstead pancreas HPLRB1"
                                       DB 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult, 34 years"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88.8; DI
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"IMAGE:1412689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex "female"
                                                                                                                                                                                                                                                                                                             AA835205.1 GI:2908933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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FEATURES

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Gaps

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BASE COUNT ORIGIN

Matches

g

RESULT

Gaps

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butharia; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 110)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu,. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search/page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             העטטטוט DNA GSS 14-APR-1999
RPCIII-1D10.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1D10,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 17561 TTTTTTTTTTTGAAATAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGCGAATCTC 17620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY 17621 AGCTCACTGCAACGTCCGCCTCCTGGGTTCAAGTGATTCTCCTGCCTCA 17669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88.2; DB 94;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPCI11 Human Male BAC Library ^{\prime\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                          1. 109
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="RPCI-11-1D10"
                                                                                                                                                        /clone="2313G15"
/clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11"
/sex="Male"
                                             Location/Qualiflers
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AQ003188.1 GI:3030392
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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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/cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library Al"
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Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1997)
Other_GSSS: 345K02.TP 345K02.TPB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: madadams@tigr.org
Clones are available from Research Genetics (Info@resgen.com). BAC
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Seg primer: M13-21
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CIT978SKA1"
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Other_GSSs: RPCIII-13414.TJ

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Fax: 301 838 0208

Email: bbeeqilgr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pleter@delpong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (http://bacpac.med.bac_end_search/bac_end_search.html
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Class: BAC ends.
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1 (bases 1 to 110)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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/db_xref="GDB:7551267"
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unpublished (1998)
Other_GSSs: CITBI-E1-2509A2.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: medicansetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
I (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Sex="maic"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11574 GGGTTTCACTTTGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGGCCCGCCTC 11633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA244245 110 bp mRNA EST 20-AUG-1997 nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence. AA244245.1 GI:1875104
                                                                                                                                                   AQ264176 106 bp DNA GSS 27-OCT-1998
CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GGGTTTCACCATGTTAGCCAGGACGTCTTGATCTCCTGACCTCGTGATCCACCCGCCTC 47
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50 TCAGCCTCCCAAAGTACTTGGATTACAGGCGTGAGCCACTGCTCCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Conservative
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KEYWORDS
SOURCE
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ORGANISM

AUTHORS TITLE REFERENCE

JOURNAL

COMMENT

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10943 TAGCTGGGCGTGGTGCCACATGCCTGTAGTCCCAGCTACTGGGGAGGCTGAGGCAGGAGA 11002
                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478 On Nov 29, 1993 this sequence version replaced 91:429999.
                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
High quality sequence stops: 101
Source: IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: MISRI
High quality sequence stop: 101.
Location/Qualifiers
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CIT-HSP-2017G2.TRB CIT-HSP Homo sapiens genomic clone 2017G2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
                                                                                                                                                                                                                                                                                   Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%; Score 85.8; DB 24; Length 107; Best Local Similarity 86.9%; Pred. No. 0.44; Matches 93; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 11003 ATTGCTTGAACTCGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGC 11049
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                      AUTHORS
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B65160/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dew_stage="45 years old"
/dew_stage="45 years old"
/lab_host="nbil0B"
/note="vector: pAMPI0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
bDNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMPI0 by the UDC-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
17 a 26 c 28 g 38 t 1 others
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                                                                                                                                                                                                                                                                                   Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmest-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: N.I.-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H67040 107 bp mRNA EST 27-0CT-1995 yu68c01.rl Weizmann Olfactory Epithelium Homo sapiens CDNA clone IMAGE:238944 5' similar to contains Alu repetitive element;, mRNA
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 110) NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Jan 24, 1995 this sequence version replaced gi:634306.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110;
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Pred. No. 0.35;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 90. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ww-bio.llnl.gov/bbrp/image/image.html
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/clone_lib="NCI_CGAP_PrI"
/sex="Male"
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source

FEATURES

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Gaps

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Query Match

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BASE COUNT

ORIGIN

DEFINITION

RESULT 13

H67040/c

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

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                                                                                                                 Other GSSS: CIT-HSP-2017G2.TFB
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
71e1: 301 838 0200
Fax: 301 838 0200
Enail: madadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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                         Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27833 TGGGCAGTGGCGTGATCTCGGCTCGCTGCAACCTCTGCCTCCCGGGTTCAAGTGATTCTC 27892
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Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1402063.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Pred. No. 0.44;
0; Mismatches 12; Indels 0;
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/db_xref="GDB:7043860"
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/sex="Male"
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AA812141.1 GI:2881752
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Best Local Similarity 88.6%;
Matches 93; Conservative 0
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                                                                                                  Unpublished (1997)
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AUTHORS
                                                                                                  JOURNAL
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Clone distribution: NCI-CGAP clone distribution information can be
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                                                                      Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 60.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.3%; Score 85.2; DB Best Local Similarity 87.7%; Pred. No. 0.52; Matches 93; Conservative 0; Mismatches
                                                          Std Error: 0.00
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Job time: 345812 sec
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APPLICATION NUMBER: US/08/481,658B
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Pred. No. 1.4e-09;
US-08-450-673C-92
PCT-US95-1711A-92
US-08-454-557C-60
US-08-340-4260-60
US-08-454-557C-60
US-08-454-557C-60
US-08-454-557C-69
US-08-454-557C-69
US-08-46-4260-69
US-08-477-504A-66
US-08-48-652B-66
US-08-48-652B-66
US-08-48-652B-66
US-08-48-652B-66
US-08-48-557C-70
US-08-48-557C-70
US-08-48-652B-66
US-08-48-557C-70
US-08-48-557C-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 65, Application US/08481658B
; Patent No. 595575
; GENERAL INFORMATION:
; APPLICANT: 2astorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
; TITLE OF INFUNTION: MN Gene and Protein
; UNMER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/481,658B FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/260,190 FILING DATE: 15-JUN-1994 ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leona L. Lauder
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STREET: 6 Mariposa Court
CITY: Tiburon
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TYPE: nucleic acid
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STRANDEDNESS: single
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COUNTRY: USA
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Best Local Similarity
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US-08-481-658B-65
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10130.052 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-340-426D-91
US-08-450-426D-91
US-08-450-426D-91
US-08-440-426D-70
US-08-440-426D-70
US-08-450-673C-70
US-08-454-557C-92
US-08-454-557C-92
US-08-340-426D-92
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US-08-486-756A-65
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US-08-481-658B-65
US-08-481-658B-65
US-08-487-504A-65
US-08-485-862B-65
US-08-485-862B-65
US-08-485-862B-65
US-08-45-576-91
US-08-450-67-91
US-08-450-67-91
US-08-450-67-91
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Listing first 45 summaries

    nucleic search, using sw model

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  Gaps
                                                      2 TITITACATCITIAGIAGACAGGGITICACCATATIGGCCAGGCIGCTCTCAAACTCC 61
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: U7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECPHONE: 415-435-3034
TELECPHONE: 415-435-3034
0; Mismatches 13; Indels
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                                                                                                               Qy 28010 TGACCTCATGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGAT 28053
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0.3%; Score 83.2; DB 4;
Best Local Similarity 87.5%; Pred. No. 1.4e-09;
Matches 91; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                US-08-477-504A-65
; Sequence 65, Application US/08477504A
; Patent No. 5972353
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TYPE: nucleic acid
STRANDEDNESS: single
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91; Conservative
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CITY: Tiburon
STATE: California
COUNTRY: USA
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US-08-477-504A-65
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Dy 27950 ITITIGIATITITATIAGAGACAGGGITICACIAIGITGGCCAGGCIGAICICAAACICC 28009
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Pred. No. 1.4e-09;
0; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING STERM: POLDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY, AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
PROTECTION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY 28010 TGACCTCATGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGAT 28053
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                                                              APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D-0021.3C
Sequence 65, Application US/08486756A Patent No. 5981711
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Patent No. 5989838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION: TELECOMMUNICATION TELEFAS: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.3%;
Best Local Similarity 87.5%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ZIP: 94920
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US-08-486-756A-65
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REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.3%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.38
Best Local Similarity 87.55
Matches 91; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic stranbedness: TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-08-787-739-65
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                                                                         COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DSyMS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT: LEONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OY 28010 TGACCTCATGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGAT 28053
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jarcmir
TITLE OF INVENTION: MN Gene and Protein
WIMMER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
CITY: San Francisco
CITY: Collifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                           D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lauder, Leona L.
REGISTRATION UNUBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INPORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                             COMPUTER READABLE FORM:
California: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 91; Conserva
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                                         94920
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US-08-485-862B-65
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US-08-787-739-65
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27950 TTTTTGTATTTTTATTAGAGACAGGGTTTCACTATGTTGGCCAGGCTGATCTCAAACTCC 28009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 28010 TGACCTCATGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGAT 28053
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Pred. No. 1.4e-09;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-481-658B-65/C
Sequence 65, Application US/08481658B
Fatent No. 5955075;
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: OCCURTATIONERS
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBARE: US 08/485,049
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION UNBARE: US 08/477,504
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-UN-1995
ATTORNEY ARBITICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-UN-1995
ATTORNEY ARBITICATION NUMBER: US 08/487,077
REGISTRATION UNMBER: 30,863
ATTORNEY ARBITICATION NUMBER: 10-0071,4
PREDISTRATION UNMBER: 30,863
PREDEDENTE ANTHRED. D-0071,4
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Gaps

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Length 105;

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24972 ATCCCAGCTCTTTGGGAGGCCTAGGCGGGTGGATCACGAGGTCAGGAGTTCAAGACCAGC 25031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORIEX APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY 25032 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAGTATAAAAA 25075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
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0.3%; Score 81.6; DB 4;
Best Local Similarity 86.5%; Pred. No. 3.1e-09;
Matches 90; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
TITLE OF INVENTION: MN GENERAL OF CORRESPONDENCES: 86
CORRESPONDENCE ADDRESS:
                                                                           D-0021.3D
                                       REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,863
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STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 105 base pairs
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                  Lauder, Leona L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415-435-0727
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US-08-486-756A-65/c
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US-08-477-504A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.3%; Score 81.6; DB 4; Length 105; Best Local Similarity 86.5%; Pred. No. 3.1e-09; Matches 90; Conservative 0; Mismatches 14; Indels (
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
APPCNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25032 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAAGTATAAAAA 25075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 CIGGCCAATATGGTGAAACCCTGTCTACTACAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-004-477-504A-65/C

Sequence 65, Application US/08477504A

Petent No. 5972353

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MW Gene and Protein
NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/477,504A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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R: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11r
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-08-481-658B-65
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCMUTER: IBM PC COMPATION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
                                                                                                   Qy 25032 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAAGTATAAAAA 25075
                                                                                                                               45 CTGGCCAATATGGTGAAACCCTGTCTTACTAAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-0021.4
                                                                                                                                                                                                                             RESULT 10
US-08-787-739-65/c
; Sequence 65, Application US/0878739
; Patent No. 6027887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-981-0332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                               105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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                                                                                                                                                  0.3%; Score 81.6; DB 4; Length 105;
86.5%; Pred. No. 3.1e-09;
tive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%; Score 81.6; DB 4; Length 105; 86.5%; Pred. No. 3.1e-09; tive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
SOFTWARE: PACENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      QY 25032 CTCGCCAAGATGGTGAAATCCCGTCTACTAAAAAGTATAAAAA 25075
                                                                                                                                                                                                                                                                                                                                                                                  45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-0021.3D
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/08485862B Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               Query Match 0.39
Best Local Similarity 86.59
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.3 Best Local Similarity 86.5 Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6 Mariposa
CITY: Tiburon
STATE: Callfornia
COUNTRY: USA
ZIP: 94920
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US-08-485-862B-65/c
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                    HYPOTHETICAL:
ANTI-SENSE:
US-08-486-756A-65
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                   24972 ATCCCAGCTCTTTGGGAGCCCTAGGCGGGTGGATCACGAGGTCAGGAGTTCAAGACCAGC 25031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY 11585 TGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGCCCCGCCTCAGCCTCCCAAA 11644
                                                                                Gaps
                                                                                                                                                                105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGAGTTTGAGAGCAGCAGC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                      Length 105;
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                                                                             14; Indels
                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,557C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: LUDWIG, SEEVEN R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 36,203

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2500

TELEFAN: (202) 371-2500
                    Score 81.6; DB 5;
Pred. No. 3.1e-09;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91, Application US/08454557C Patent No. 5830670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 91, Application US/08340426D
; Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oy 11645 GTGCTGGGATTACAGGAGTG 11664
                      ch 0.3%;
1 Similarity 86.5%;
90; Conservative
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Matches 72; Conservative
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                      Query Match
Best Local
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                                                                             Matches
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Sequence 91, Application US/08450673C
Patent No. 594888
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Allzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 11585 TGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGGCCCGCCTCAGCCTCCCAAA 11644
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Pred. No. 4e-06;
0; Mismatches 8; Indels
                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: Washington STATE: D.L.
                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/340,426D FILING DATE: 14-NOV-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GTGCTGGGATTACAAGCGTG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%;
Best Local Similarity 90.0%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
US-08-340-426D-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-450-673C-91
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8; Indels

0.2%; Score 67.2; DB 6; 90.0%; Pred. No. 4e-06; tive 0; Mismatches 8;

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DY 11585 TGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGCCCCCCAGCCTCCCAAA 11644
                                                                                                                                                                                                      Qy 11645 GTGCTGGGATTACAGGAGTG 11664
                                                                                   Query Match 0.2%
Best Local Similarity 90.0%
Matches 72; Conservative
  TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     both
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US-08-454-557C-91/C
                    PCT-US95-17111A-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-454-557C-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 91, Application PC/TUS9517111A

Sequence 91, Application PC/TUS9517111A

GENERAL INFORMATION:

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Detection of Alzheimer's Disease

TITLE OF INVENTION: Detection of Alzheimer's Disease

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%; Score 67.2; DB 4; Length 84; 90.0%; Pred. No. 4e-06; tive 0; Mismatches 8; Indels
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ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
           APPLICATION NUMBER: US/08/450,673C
CLASSIFICATION: S10
CLASSIFICATION: S10
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
INFORMATION FOR SEO ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
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REGISTRATION NUMBER: 36,203
REFERENCE_TOOKET NUMBER: 0609.3840002
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILLING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 90.0%
Matches 72; Conservative
CURRENT APPLICATION DATA:
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STRANDEDNESS: both
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PCT-US95-17111A-91
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US-08-450-673C-91
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Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
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ZUP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
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NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,203
REFERENCE/COCKET UNDRER: 0609
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
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64 GTGCTGGGATTACAAGCGTG 83
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STRANDEDNESS: both
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Search completed: June 18, 2000, 17:46:45 Job time: 363135 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 110
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KEYWORDS
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Direct Submission

Direct Cloud (22-AdG-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Jases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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                            HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L.
CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Homo sapiens
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0.3%; Score 96.6; DB 9;
Best Local Similarity 96.1%; Pred. No. 2.3e-09;
Matches 99; Conservative 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="embryo"
/sex="male"
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30 c 35 g 1
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/db_xref="taxon:9606"
/clone="TscAlu2"
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/rpt_family="Alu"
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                                                                                                                                                                   Gaps
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Primates; Catarrhini; Hominidae; Homo.
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Alu repetitive sequence; low density lipoprotein receptor.
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Alu repetitive sequence; low density lipoprotein receptor.
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Human LDL-receptor gene intron 14 fragment (normal gene).
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See Kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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1 Similarity 89.5%; Pred. No. 1.5e-07;
94; Conservative 0; Mismatches 11;
                                                                                                                Score 89; DB 11; I
Pred. No. 7.4e-08;
); Mismatches 5;
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23 c 39 g 18 t
                                                                                                                                                              0; Mismatches
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/db_xref="taxon:9606"
1. 108
/rpt_type=dispersed
39 c 30 g
                                                                                                                0.3%;
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Matches 92; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)
Sinnert, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Jases 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Homo sapiens
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Pred. No. 2.4e-06;
0; Mismatches 11;
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27 c 33 q 1
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/db_xref="taxon:9606"
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Best Local Similarity 88.9%;
Matches 88; Conservative
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1 (bases 1 to 108)
Horsthemke, B., Balsiegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
Eur. J. Blochem. 164 (1), 77-81 (1987)
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1 (base) 1 to 107)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Blol. (1992) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
1. 108
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 108
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Pred. No. 2e-07;
0; Mismatches 12;
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Pred. No. 3.9e-07;
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23 c 39 g 18 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="RTera2b1"
/dev_stage="embryo"
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30 c 35 g 1
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Best Local Similarity 88.7%;
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shalkh.T.H., Kim.J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human LDL-receptor mutated gene with intron 12 deletion junction. x05249. x05249. GI:34335
             16540 CTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTGTCTCCAGGGTTCAAGCGAT 16599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10871 GTAGAGACAGGGTTTCACCGTGTTGGCCAGGATGTTCTCAATCTCCTTACCTCGTGATCC 10930
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                                           103 CTGGAGTGCAATGGCACGATCTCGGCTCACTGCAACCTCCGGCTTCCAAGCGAT 44
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 108)
Shalkh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 GTAGAGACGGGGTTTCACCTTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 38
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Pred. No. 2.9e-06;
0; Mismatches 10; Indels
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                                                                              16600 TCTCCTGCTTCAGCCTATGGAGTAGCTGGGATTACAGGC 16638
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                                                                                                43 TCTCCTGCCTTAGCTTCCCGTGTAGCTGGGATTACAGGC 5
                                                                                                                                                                                       нsU67803 108 bp RNA
Human small cytoplasmic Alu transcript.
U67803
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97415756
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1.108
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
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/rpt_type=dispersed
39 c 30 g
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Matches 87; Conservative
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*Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
all-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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1 (Bases 1 to 108)

1 (Bases 1 to 108)

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for Eur. J. Blochem. 164 (1), 77-81 (1987)
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See X0520 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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/cell_type="blood leukocytes from a patient with familial"
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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m c} 20 g t
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Pred. No. 4.6e-06;
0; Mismatches 15;
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20 c 40 g 20 t
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/organism="Homo sapiens"
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Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 84.8%;
Matches 89; Conservative
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
                                                                      11838 TCGGCTCACCGCAACCTCCGCCTCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCCA 11897
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Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                                                                  47 GTAGCTGGGATTACAGGCACCTGCCACCACCACGCTAATTTT 4
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84.8%; Pred. No. 6.1e-06;
tive 0; Mismatches 16;
                                      15;
0.3%; Score 80; DB 10;
35.6%; Pred. No. 4.6e-06;
                                    0; Mismatches
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               85.68;
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See X05250 for corresponding normal gene sequence
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryotz, Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (Bases I to 108)

1 (Bases I to 108)

1 (Bases I to 108)

Williamson,R. and Humphries,S.

Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Pred. No. 6.1e-06;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
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/db_xref="taxon:9606"
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Direct Submission
Submitted (22-AdC-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                        11838 TCGGCTCACCGCAACCTCCGCCTCCAGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCCCA 11897
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                                                                                         2 TCGCCTCACCACAACCTCTGCCTCCTGGGTTCAAACCATTTTCCTGCCTCAGCCTCTA 61
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Homlinidae; Homo.
1 (bases 1 to 108)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M. A. and Deininger, P. L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Human carcinoma cell-derived Alu RNA transcript, clone CE272.
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 Length 108;
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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                                       18; Indels
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0.3%; Score 78.2; DB 10;
83.2%; Pred. No. 1.1e-05;
tive 0; Mismatches 18;
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Human small cytoplasmic Alu transcript.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu3"
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/rpt_family="alu"
/rpt_type=dispersed
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum DB seq length: 110
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9333 GGAGGCCGAGGCGGCGGATCACGAGGTCAGGAGAT 9368 GGAGGCCGANACGGGCGGATGACGAGGTCAGGAGAT

32/c T24892 standard; cDNA to mRNA; 100 BP.

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RESULT T24892/ ID T2

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Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Holymorphism: biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease, cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.

Homo sapiens

WO9820165-A2.

H4-MAY-1998

O5-NOV-1997; U20313.

O6-NOV-1997; US0313.

WHIDHEAD INST BIOMEDICAL RES.
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                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease testing or phenotypic typing for disease claim 1; Page 219; 310pp; English.
            05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
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78.8%; Pred. No. v..
78.9%; O; Mismatches
                                                                                                cell typing; abnormal cell function; ss. Homo sapiens.
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Best Local Similarity 78.8
Matches 78; Conservative
                                                                                                                                                            01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                   Okubo K;
                                                                                                                                                                                                                                                                                       WPI; 95-206931/27
                                                                                                                                                                                                                                                                        Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                          tissues
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X12095
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markers which have been isolated using the primers represented in markers which have been isolated using the primers represented in the markers which have been isolated using the primers represented in the 209121-340268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in a sagammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy. Wiskott-Addrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Bhiers-Danios syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous such autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, and only pathogenic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human gene claim 37; Page 18; 60pp; English.

Claim 37; Page 18; 60pp; English.

Sequences shown in V4120 to V4124/ represent nucleotide sequences of sequences shown in V4120 to V4124/ represent nucleotide sequences of mouse EST from tagged cDNA clones. These are used in the method of the invention of screening for human developmental genes. The method comparises inserting a promoterless reporter gene into a non-primate mammalian embryonic stem cell (ESC) genome and identifying cellular transcripts that encode the reporter gene product. Fragments of genes encoding these transcripts are cloned and sequenced. A gene encoding the transcript, or part of it, in different evel of the gene encoding the transcript, or part of it, in different cell types and/or different developmental stages is detected. A gene showing different are encoding its selected and expression levels of a homologous non-human primate gene, in different cell types and/or at differential expression is selected and the non-primate transcript as probe is detected. A homologous gene having the same pattern of differential expression is selected and the non-primate gene, or part of it is used to identify the homologous human gene. The ESC transcripts identified by this method are used to generate transgenic animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11941 TGTATTTTTATTAGAGATGAGGTTTCTCCATGTTGGTCAGACTGGTCTCGAACTGCCGAC 12000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for human developmental genes - by trapping in murine embryonic stem cells and analysing differential expression in vitro, selecting homologous non-human primate gene and using it to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.2%; Score 66.8; DB 1; Length 108; 81.5%; Pred. No. 0.01; Live 1; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1998 (first entry)
Mouse embryonic cell EST 13-4 nucleotide sequence.
Embryonic stem cell, ESC; non-primate; mouse; EST; human;
developmental gene; transgenic animal; reporter gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-00V-1997; U22335.
27-NOV-1996; US-032510.
(CORR) CORNELL RES FOUND INC.
HOLZSCHU DL, MARK WH;
WPI; 98-322656/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V41231 standard; cDNA; 86 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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V41231

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selected from rats, hamsters, rabbits, dogs, pigs, horses, cows, monkey, babbon or chimpanzee for study of gene function. The method provides rapid and large scale screening for human developmental genes, and eliminates the need to analyse reporter gene expression in embryos. Sequence 86 BP; 16 A; 28 C; 30 G; 12 T;
                                                                                                                                                                                       19115 CTTTTGGGGCGTGTGACCATCGCGCAGGTGGCGTTTTGCCTAATATTCAGGCGGTGCTG 19174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2895 ATGCCATGAACCTGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAA 2954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented conna hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                           2 CTGCTGGGCCGTGTGACCATCGCGCAGGCGCGCTCCTGCCCAATATCCAGGCCGTGCTG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ATCGCTTGAACCTGGGAGGCAGAATTTGCAATNAGCTGAGATTGCACCNTTGCACCTCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS acquences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsubara K, Okubo K;
WPI; 95-206931/27.
Tdentifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                     Query Match 0.2%; Score 63.8; DB 1; Length 86; Best Local Similarity 85.5%; Pred. No. 0.031; Matches 71; Conservative 0; Mismatches 12; Indels
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Pred. No. 0.029;
0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGGGAGACACAGGGAGACTCCGTCTCAAAAAAAAAA 2993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CCTGGGTGACAGAGTGACACTCTGTTTGAAACAAAA 100
                                                                                                                                                                                                                                                                                                                                                                               124892 standard; cDNA to mRNA; 100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1720; 2245pp; Japanese,
                                                                                                                                                                                                                                                           19175 CTGCCTAAGAAACTGAGAGCCA 19197
                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                           62 CTGCCCAAGAAGACGGAGAGCCA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.2
Best Local Similarity 76.8
Matches 76; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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Claim 1; Page 758-759; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

C double-stranded DNA) which comprises one of the 7837 "GS sequences

given in T19001-T26837 and which is able to hybridise to part of

thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

curranslated sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

c is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

C The appearance frequency of a given GS in a cDNA library can be

c determined (esp. using primers and probes derived from the GS.

Sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10793 GATTCTACTGCCTCGCCCTCCCGAGTAGCTGGGACCACAGATACGTGCCCACCATGCCCCG 10852
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Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Human biallelic, human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autolimnue disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                          24-JUL-1996 (first entry)

Human gene signature HUMGS02180.

Gene signature: messenger RRMs, mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           function, by preparing cDNA that corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA thar reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 0.045;
0; Mismatches 24;
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
HUGSON T, Lander ES, Wang D;
WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 C;
standard; cDNA to mRNA; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recognising different cell types. Sequence 103 BP; 22 A; 27
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                                                       (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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T20927
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The restriction of properties of the contain belong the containing polymorphic forms for use in e.g. forensics, paternity by testing or phenotypic typing for disease

Claim 1: Page 219; 310pp; English.

CX 10269-XI2937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-XI0268 The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, c.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, hereditary spherocytosis, von Willebrand's disease, thereditary captemorthagic telangiectasia, familial colonic polyposis, Ehlers-Danlos Syndrome, osteogenesis imperfected, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such cautoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics can slongevity, appearance (e.g. baldness, obseity), strength, speed, candurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid connowlaxis of such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7108 TTAATCCCGGCAATTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCGGGAGTTCGAGA 7167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T1901-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from warious human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs species, almost different mRNAs is a couracted to a constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
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WO9514772-A1.
isolated nucleic acid seqments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsubara K, Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 108;
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Pred. No. 0.045;
1; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1996 (first entry)
Human gene signature HUMGS07131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis of such diseases.
Sequence 108 BP; 19 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2
Best Local Similarity 76.0
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T25009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A single-stranded DNA (or its complementary strand or the corresp. a single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS sequences of given in T19001-T25687 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end ranslated sequence is unique to a particular mRNA species, almost is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 93 BP; 25 A; 27 C; 24 G; 17 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13277 TTTGAGATGGAATTTCACTCTTGTTGTTGTCAGGCTGGGGTGCAGTGGCACAGTCTCAGCTC 13336
                                                                                                                                                                                                                    10694 TTTTTTTGAGACTGAGCCTTGCTCTGTCACCCAGGCTGGAGTGCAATGGCGCG 10753
                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                        103 TGTTGTTGTTTTCAACAGGGTCTTGCTCTGTCACTCAGGCTGGAATNCAGTGGCGTG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
                                                                                                                                       Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 93;
                                                                                                                                                                            26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                                              10754 ATCTCGCCTCACTGCAACCTCCGCTTCCAGGTTCAAGCGAT 10795
                                                                                                                                                                                                                                                                                                                 43 ACCATGGCTCACTGGCCTTGGGCTCATGGCGTAT 2
                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                          Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.13;
                                                                                                                                                                            0; Mismatches
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0; Mismatches
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                                                                                                                                           Score 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGTGGCTTCGGCTTCCTGGGCTCAAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               T25688 standard; cDNA to mRNA; 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-ocr-1996 (first entry)
Human gene signature HUMGS07887.
                                                                                                                                       0.2%;
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Best Local Similarity 75...
72; Conservative
                                                                                                                                       Query Match 0.29
Best Local Similarity 74.59
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MAT'S.) MAT'SUBARR K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 95-206931/27.
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isolated nucleic acid segments from the human genome - used
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WO9820165-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded DNA for its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of pure of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
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Human biallelic polymorphic DNA fragment EST98276a.
Polymorphism: biallelic; human; forensic; paternity testing; disease; detection; phenotyping; characteristic; infection; hereditary; autofimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%; Score 60.2; DB 1; Length 108; 72.0%; Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CCTGAGTGACAGAGCAGAGACCTGTTGAAAACAACAACAACAACAAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                           T25009 standard; cDNA to mRNA; 108 BP.
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(WHED) WHITHEAD INST BIOMEDICAL RES.
HUGSON T, Lander ES, Wang D;
WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japanese.
                                                                                                                                                             07-NOV-1996 (first entry)
Human gene signature HUMGS07131.
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ID X12087 standard; DNA; 100 BP.
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Matches 77; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okubo K;
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14-MAY-1998.
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                         RESULT
T25009
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The Manual Manua
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Polymorphism: biallelic; human: forensic; paternity testing; disease; detection; phenotyphic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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Pred. No. 0.17;
1; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8494 CCAGGAGCTCAAGACCAGTCTGGGCAACTTAGTGAGAC 8531
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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Sequence 100 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X12085 standard; DNA; 100 BP.
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Best Local Similarity 74.59
Matches 73; Conservative
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BP.

75

61 CCCCATTCCTCACTT

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RESULT 14

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autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments an also be used to produce medicaments for the treatment or prophylaxis of such diseases. 25 C; 22 G; 30 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12008 GATCCACCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTATGAGCCACTGGGCCCGG 12067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8434 TGCAGCTCACGCCTGTAATACCAGCATTTTGGGAGGCCAAGGTGGGAGGATCACTTGAGC 8493
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sequence 110 BP; 22 A; 7 C; 28 G; 17 T;
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WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                   Length 100;
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                                                                                                                                                                                                                                                                                                                                                               Score 59.2; DB 1;
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 CCAGGAGCTCAAGACCATCCTGGGAAACATAGCAAGAC 3
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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The standard with the segments and the standard sender of the standard segments are standard segments. The standard segments are claim 1; page 219; 310pp; English.

X10269-XX2937 are human DNA fragments which contain biallelic polymorphic testing or phenotypic typing for disease coupying the primers represented in X09121-XX10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic syndrome, reachers in polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, hereditary cancer, observing, appearance (e.g. familial colonic polyposis, Bhiers Danios syndrome, osteogenesis inperfected, acute intermittent porphyria, autofimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic or determine of each of such a produce medicaments for the treatment or proposition of such an entermine of the content of the cont
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                                                                      Human biallelic polymorphic DNA fragment EST98276b. Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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                                                                                                                                                                                                                                                                                                                                (WHED ) WHITEHEAD INST BIOMEDICAL RES.
Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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Homo sapiens.

01-JUN-1995.
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Pred. No. 0.27;
0; Mismatches
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Human gene signature HUMGS07421.
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Best Local Similarity /*..
And 73; Conservative
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X12086 standard; DNA; 100
X12086;
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06-NOV-1996; US-030455.
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double-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in 19001-172837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
sequence 110 BP; 34 A; 27 C; 23 G; 20 T;
                                                                                                     Matsubara K, Okubo K;
WPI: 95-206931/27
Identifying gene signatures in 3'-directed human cDNA library - e.g.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
Identifying gene signatures in 3'-directed human cDNA that
reflects relative abundance of corresp. mRNA in specific human
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKDS/) OKUBO K.
Matsubara K, Okubo K;
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ô 0; Gaps Query Match

0.2%; Score 57.4; DB 1; Length 110;
Best Local Similarity 84.2%; Pred. No. 0.34;
Matches 64; Conservative 0; Mismatches 12; Indels C 12; Indels

Qy 11829 GGTGCGATCTCGGCTC 11844

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Listing first 45 summaries
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em_est14::
em_est14::
em_est14::
em_est14::
em_est15::
em_est15::
em_est17::

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em_est11:*
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9b_est16:*
9b_est18:*
9b_est19:*
9b_est19:*
9b_est20:*
9b_est21:*
9b_est24:*
9b_est24:*
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em_est4:*
em_est5:*
em_est6:*
em_est7:*
em_est8:*
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Maximum DB seq length: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                           EST: *
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                                                                                                                                                                                                                                    Scoring table:
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Contact: Wilson RK
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Matches 101;
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                                                                                           source
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AA703692/c
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ORIGIN
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A0677292 RPCI-11-4
AA44259 zv68b02.r
AA516339 ng71g02.s
AA565533 nk42b11.s
                                                                                                                      AQ264176 CITBI-EI-
AA385808 EST99495
AA807460 mx08b05.s
AW250394 2822460.3
AA703692 ag81a10.r
                                                          AAA43009 zr25h02.s
AAB43009 zr25h02.s
AAB97366 am06h02.s
AA828124 od71a07.s
N49638 yv25e09.r1
AQ076649 CIT-HSP-2
AA226656 nc19f09.s
                                                                                                                                                                                                                                                       N23686 yw46a02.s1
AQO38426 CIT-HSP-2
AQO3188 RPCII.D
AA654562 nt75fl0.s
AM19512 xm06e06.x
A193497 wm74d02.x
A1168167 co09e10.x
A1770029 EST81584
AA564832 nj22a06.s
AQO28649 CIT-HSP-2
             AA243009 zr25h02.s
AA703692 ag8la10.r
A1832832 at72g09.x
A8812141 ob48h02.s
B48914 RPCIII.4A12
                                                                                                                                                           AO544957 CITBI-E1-
H67040 yu68c01.rl
                                                                                                                                                                                                           AQ582186 RPCI-11-4
                                                                                                                                                                                                                                                                                                                                  AQ584425 RPCI-11-4
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ob48h02.s
CIT-HSP-2
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AW083640 xc49f02.x
B48914 RPCI11-4A12
                                                    AA835205 ak64h01.s
                                                                                                                                                                                           B17434 345K2.TVB C
AQ003188 RPCI11-1D
                                                                                                                                                                                                                                                                                                                                                                                                              AA243009 109 bp mRNA EST 11-MAR-1998 zr25h02.s1 Stratagene NT2 neuronal precursor 937230 Homo saplens cDNA clone IMAGE:664467 3' similar to contains Alu repetitive element;contains element LTR1 repetitive element; mRNA sequence. AA243009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)

On Dec 3, 1996 this sequence version replaced gi:1126869.
Description
                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                 AQ584425
AA583697
                                                                                                                AA226656
AQ264176
                                                                                                                                      AA807640
AW250394
AA703692
AO544957
                                                                                                                                                                                                  AQ003188
AQ582186
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AI933497
                                                                                                                                                                           AW083640
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                                                                                   AA828124
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DB
Length
Match
               human.
              82.4
82.5
82.2
82.2
81.8
82.8
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VERSION
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JOURNAL
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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 106)
S. Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Leacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Thaising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397630.
Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This Clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1127 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 102.
Location/Qualifiers
1. 109
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 CACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGGCGGATCACGAGGTAGGGAGAT 50
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9369 GGAGACCATCCTGCTTAACACGATGAAACCCCGTCTCTACTAAAAATAC 9417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96.2; DB 3
Pred. No. 0.076;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.3%; Scur-
92.7%; Pred
0; V
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AA703692.1
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TITLE
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KEYWORDS
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                                                                                                                                                  /db_xref="taxon:9906"
/db_xref="taxon:9906"
/clone_"lb="stratagene hhr neuron (#937233)"
/dev_stage="hhr neurons"
/dev_stage="hhr neurons"
/dev_stage="hhr neurons"
/dev_stage="hhr neurons"
/dev_vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: CoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: CoRI; Site_2:
/note="Vector: pBluescript SK-; Site_2: CoRI; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at72g09.xl Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377600 3' similar to contains Alu repetitive element; contains element MER22 repetitive element i, mRNA sequence. AI832832
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.3%; Score 94.8; DB 37; Best Local Similarity 93.4%; Pred. No. 0.11; Matches 99; Conservative 0; Mismatches 7;
Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 53. Location/Qualifiers
                                                                                                                             /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: WCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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1 (bases 1 to 106)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                DY 11788 GAGAGGAGTTTCACACTTGTTGCCCAGGCTGGAGTGCAATGGTGCGATCTCGGCTCACC 11847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
On Sep 12, 1996 this sequence version replaced gi:1402063.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                            Score 93.8; DB 61; Length 105;
Pred. No. 0.14;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1334643"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                           7;
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Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 60.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 93.33
Matches 98; Conservative
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Pred. No. 0.24;

4

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93.28;
                    Conservative
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Matches 95; Conser
     Best Local Similarity
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AA835205/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Email: mdadams@tigr.org
Email: mdadams@tigr.org
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (http://bacpac.med.bufgen.com). BAC end search/pac_end_search.html
Seg primer: SP6
Class: BAC ends.
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1 (bases 1 to 103)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                     9481 GGAGAATGGCGTGAACGCGGGGGGGGGGTTGCAGTGAGCCGAGATCGCGCCACGGCAC 9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               B48914 103 bp DNA GSS 08-APR-1999 RPCIII-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12, genomic survey sequence.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                           106 GGAGAATGGTGTGAACCTGGGAGGTGGAGCTTGCAGTGAGCCGAGATCACACACTGCAC 47
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                                                                                                                                                                                               Length 106;
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Pred. No. 0.17;
0; Mismatches 8;
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/db_xref="GD8:7501163"
/db_xref="taxon:9606"
/clone="RRCI-11-4A12"
/clone_lib="RRCI-11"
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1. .103
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B48914.1 GI:2601151
                                                                                                                                                                                                                  Best Local Similarity 92.5
Matches 98; Conservative
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AUTHORS
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Score 91.8; DB 84; Length 103;

0.3%;

Query Match

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3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "

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with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
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IMAGE:1412669 3' similar to contains Alu repetitive
element; contains element KER repetitive element ;, mRNA sequence.
AA835205
AA835205.1 GI:2908933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marthi, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thaising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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                                                           9316 GTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAGATGGAGACC 9375
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                                                                                         23-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:636191.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.27;
0; Mismatches 6; Indels 0;
     Indels
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/clone_lib="Barstead pancreas HPLRB1"
/sex="female"
                                                                                                                                                                            9376 ATCCTGCTTAACACGATGAAACCCCGTCTCTACTAAAATACA 9418
                                                                                                                                                                                                            61 ATCCCGCTAAAACGGTGAAACCCCGTCTCTACTAAAAATACA 103
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     7;
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        Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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ilarity 94.1%;
Conservative (
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DEFINITION

N25299/c

RESULT

8

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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AA897366 110 bp mRNA EST 04-JAN-1999 am06h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466067 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                            AA243009 109 bp mRNA EST 11-MAR-1998
2251002.31 Strategene NT2 neuronal precursor 937230 Homos saplens
cDNA clone IMAGE:66467 3' similar to contains Alu repetitive
element;contains element LTR1 repetitive element ;, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,P., Wylle,T., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 316 280
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/db_xref="GDB:5426481"
/db_xref="CDB:5426481"
/db_xref="taxon:9506"
/clone="ImAGE:664467"
/clone=lib="Stratagene NT2 neuronal precursor 937230"
/dev_stage="neuroepithelial cells"
/dev_stage="Neter-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTATTTTTAGTAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTTGATCTCCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Dec 3, 1996 this sequence version replaced gl:1126869.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 91.4; DB 30; Length 109; Pred. No. 0.26;
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/tissue_type="olfactory epithelium" |
/tissue_type="15 year old" |
/dev_stage="35 year old" |
/dev_stage="35 year old" |
/dev_stage="35 year old" |
/dev_stage="15 ye
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1 (bases 1 to 109)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riklin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thterry Meg,J., Parson,F., Theory,B., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                    N25299 109 bp mRNA EST 28-DEC-1995
yw52c09.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone
IMAGE:255856 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
Source: IRAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mi3 -40 forward
High quality sequence stop: 307.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 109;
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/clone="IMAGE:255856"
/clone_lib="Weizmann Olfactory Epithelium"
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Pred. No. 0.24;
0; Mismatches 12;
1. .109
/organism="Homo sapiens"
/db_xref="GDB:3866265"
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Best Local Similarity 89.05
Matches 97; Conservative
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FEATURES

BASE COUNT

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96; Conservative
      Tumor Gene Index
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                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 110) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                     Unublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150764.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoelimage.llnl.gov) for further information. Insert Length: 834 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 63.
Location/Qualifiers
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1 Similarity 91.5%; Pred. No. 0.24;
97; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
/db_xref="taxon:9666"
/clone="lmAGE:146667"
/clone=lib="Scares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                      GI:3033986
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Best Local Similarity
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/note-"Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383.
                                                                                                                                                                                                                                                                         Sequencing Center
information can be
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liver spleen lNFLS Homo sapiens cDNA clone
to gb:X57138_rnal HISTONE H2B.2 (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1899815.
Contact: Robert Strausberg, Ph.D.
Tel:: (301) 496-1550
Email: Robert_Strausberg@hih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Celone distribution: NCT-GGAP clone distribution information of found through the I.M.A.G.E. Consorttum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:693230.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.2; DB 39; Length 107; Pred. No. 0.27; 0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:1373364"
/clone_lib="NCI_CGAP_OV2"
/sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 93. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="ovary"
/lab_host="DH10B"
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yv25e09.rl Soares fetal
IMAGE:243784 5' similar
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Unpublished (1998)
Other_GSSS: CIT-HSP-2363C23.TF
Other_GSSS: CIT-HSP-2363C23.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Contact and an adams@tigr.com
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 101)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Bassy,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Homo sapiens genomic clone 2363C23,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                    /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No. 0.46;
0; Mismatches 8;
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                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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EMANGALS, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhin; Hominidae; Homo.

El (bases 1 to 103)

Adams, M.D., Rounaley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.G.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

At Unpublished (1998)

Other GSSs: CIT-HSP-2323P12.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fex: 301 838 0200
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
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CIT-HSP-2323P12.TR CIT-HSP Homo sapiens genomic clone 2323P12,
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/cLone_liMAGE:243784"
/cLone_lib="Soares fetal liver spleen lNFLS"
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    .97
    /organism="Homo sapiens"

                                                                                                            Seq primer: T7
High quality sequence stop: 1.
Location/Qualifiers
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AQ028649.1 GI:3268871
                                                                                                                                                                                                                                                                                                       /sex="male"
Tel: 314 286 1800
Fax: 314 286 1810
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AQ028649
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Noticedap http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1297695.
Context: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: W Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                           9484 GAAIGGCGIGAACGCGGGAGGCGGAGCTIGCAGTGAGCCGAGATCGCGCCACGGCACTCC 9543
                                                                                                                                                                   101 GAATGGCGTGAACCCAGGAGGACGGAGCTTGCAGTGAGCCGAGATCGCGCCAATGCACTCC 42
                                                                                                                                                                                                                                                                                                                                                                         AA226656 102 bp mRNA EST 21-AUG-1997 nc19f09.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008617 similar to contains Alu repetitive element;, mRNA sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8
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Seg primer: -1mml3 fwd. ET from Amersham
High quality sequence stop: 82.
Location/Qualifiers
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/clone="InAGE:1008617"
/clone=lib="NCI_CGAP_PrI"
/sex="Male"
                                                            Score 88.2; D
Pred. No. 0.6;
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/lab_host="DH10B"
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                                                          Cch 0.3%;
al Similarity 92.1%;
93; Conservative
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Department of Edwaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research Genetics (info@resgen.com). BAC
Glones are available from Research Genetics (info@resgen.com). BAC
The Institute Institute
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1 (bases 1 to 106)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)

Other_GSSS: CITBI-EI-2509A2.TR
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
30 c 34 g 17 t
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                                                                                                                                                                               9478 GCAGGAGAATGGCGTGAACGCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCACGG 9537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ264176 106 bp DNA GSS 27-OCT-1998 CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2, apenomic survey sequence. AQ264176 GI:3792743
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                             102 GCAGNAGAATGGGATGACCCGGGGGGGGAAGCTTGCAGTAAGCCGGAATCGCGCCACTG 43
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    DB 30; Length 102;
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                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9538 CACTCCAGCCTGGGTGACAGAGCGAGACTCCGTCTCAAAAA 9579
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0.3%; Score 88.2; Di
91.2%; Pred. No. 0.6;
tive 0; Mismatches
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/db_xref="taxon:9606"
/clone="2509A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CITBI-E1"
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Best Local Similarity 89.6
Matches 95; Conservative
                                                                                            93; Conservative
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                                              Best Local Similarity
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Search completed: June 18, 2000, 22:02:37 Job time: 379524 sec

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION NATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
NAME: Lauder, Leona L.
RESISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 80; DB 4; Length 105; Pred. No. 9.5e-10;
US-08-340-426D-91
US-08-450-673C-91
DS-08-454-557C-92
US-08-340-426D-92
US-08-450-673C-92
US-08-450-673C-92
US-08-454-557C-60
US-08-35-17111A-92
US-08-454-557C-60
US-08-450-673C-60
US-08-450-673C-60
US-08-450-673C-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Application US/08481658B; Patent No. 5955075; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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85.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
    California
: USA
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Best Local Similarity
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US-08-481-658B-65
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10103.987 Million cell updates/sec
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                                                                                                                                                                                                         1 TCAAACTCCTGACCTCATGA......ATAAATATCTTTAAAATACC 29001
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Sequence 6
                                                                                                            June 18, 2000, 17:46:45; Search time 373.09 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/RCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-454-557C-69
US-08-340-426D-69
US-08-450-673C-69
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US-08-481-658B-65
US-08-48-756A-65
US-08-486-756A-65
US-08-787-739-65
US-08-787-739-65
US-08-340-4260-91
US-08-450-673C-91
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US-08-454-557C-92
US-08-340-426D-92
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PCT-US95-17111A-92
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US-08-454-557C-91
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US-08-340-426D-57
US-08-450-673C-57
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US-08-486-756A-65
US-08-485-862B-65
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        230463 seqs, 64992525 residues
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Listing first 45 summaries

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 110
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                                                                                OM nucleic
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US-08-486-756A-65

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Qy 10857 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCCAGGATGTTCTCAATCTCC 10916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,504A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRICA APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: LAUGHC, LOGNA L.

REFERENCE/DOCKET NUMBER: D-0021.3D

TELECHONE: 415-435-2034

TELEFRAX: 415-435-2034
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Pred. No. 9.5e-10;
); Mismatches 15; Indels
0; Mismatches 15; Indels
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                                                                                                                                     10917 TTACCTCGTGATCCGCCCGCCTCGTCCTGCCAAAGTGCTCGGAT 10960
                                                                                                                                                        62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAGTGCTGGGAT 105
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Best Local Similarity 85.6%; Pred. No. 9.5e-
Matches 89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF EXQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            Sequence 65, Application US/08477504A
Patent No. 5972353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...ureSSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
89; Conservative
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US-08-477-504A-65
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Matches
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RESULT

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QY 10857 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGGATGTTCTCAATCTCC 10916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
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Best Local Similarity 85.6%; Pred. No. 9.5e-10;
Matches 89; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QY 10917 TTACCTCGTGATCCGCCCCCCTCGTCCTGCCAAAGTGCTCGGAT 10960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/08485862B; Patent No. 5989838; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Laude
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 105 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                : 94920
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                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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10857 ITITIGIAITITIAGTAGAGACAGGGITICACCGTGTTGGCCAGGAIGITCICAAICICC 10916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80; DB 5; Length 105;
Pred. No. 9.5e-10;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY 10917 TTACCTCGTGATCCGCCCCGCCTCGTCCTGCCAAAGTGCTCGGAT 10960
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: GMATIPOSA COURT
                          FILING DATE: 24-0AN-1997
FILING DATE: 24-0AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-UNN-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-UNN-1995
PRIOR APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-UNN-1995
FRIOR APPLICATION NUMBER: US 08/481,658
FRIING DATE: 07-UNN-1995
FRIOR APPLICATION NUMBER: US 08/485,863
FRIING DATE: 07-UNN-1995
UMBER: US/08/787,739
24-JAN-1997
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US-08-481-658B-65/c
; Sequence 65, Application US/08481658B
; Patent No. 5955075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.3%;
85.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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CITY: Tiburon
STATE: California
COUNTRY: USA
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                                                                                                  CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURSENT PAPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
APPLICATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                     California
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Best Local Similarity
Matches 89; Conserv
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US-08-485-862B-65
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US-08-787-739-65
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Lauder, Leona L.
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US-08-477-504A-65
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                                                                                                             OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76.2; DB 4; Length 1 Pred. No. 7.3e-09; 0: Mismatches 18; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: O7-JUN-1995
CLASSIFICATION: 4.24
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US-08-477-504A-65/C
Sequence 65, Application US/08477504A
Sequence 65, Application US/08477504A
PERENT INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-UNN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UNN-1994
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.3%;
Best Local Similarity 82.9%;
Matches 87; Conservative (
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US-08-481-658B-65
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9319 ATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAGATGGAGACCATC 9378
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9379 CTGCTTAACACGATGAAACCCCGTCTCTACTAAAATACAAAATA 9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 CTGGCCAATATGGTGAAACCCTGTCTTACTAAAGATGTAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
0.3%; Score 76.2; DB 4;
Best Local Similarity 82.9%; Pred. No. 7.3e-09;
Matches 87; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ITILE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                        D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET UNMBER: D-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,863
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TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                               LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                   2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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US-08-486-756A-65/c
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9319 ATCCCAGCACTTTGGGAGGCCGAGGCGGGGGGATCACGAGGTCAGGAGATGGAGACCATC 9378
                           105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Petentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/787,739
                                                                                 9379 CTGCTTAACACGATGAAACCCCGTCTTACTAAAAATACAAAATA 9423
                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: San Francisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/78/,739
FILING DATE: 24-JAN-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/47/,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: LAUGET, LEGORA L.
RREFERENCE/DOCKET NUMBER: D-0021.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIE: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       Sequence 65, Application US/0878739; Patent No. 6027887; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-787-739-65/c
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US-08-787-739-65
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                                                                                                                                                                0; Gaps
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                                                                                                                    Score 76.2; DB 4; Length 105;
Pred. No. 7.3e-09;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.3%; Score 76.2; DB 4; Length 105; Best Local Similarity 82.9%; Pred. No. 7.3e-09; Matches 87; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/250,190
FILING DATE: 15-JUN-1994
ATTONEY/ACENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELEFAN. 415-435-2034
TELEFAN. 415-435-2034
                                                                                                                                                                                                                                                                                   9379 CTGCTTAACACGATGAAACCCCGTCTTACTAAAAATACAAAATA 9423
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                    Query Match 0.3%;
Best Local Similarity 82.9%;
Matches 87; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Leona L. Laude
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                    ; HYPOTHETICAL:
; ANTI-SENSE: N
US-08-486-756A-65
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Sequence 91, Application US/08454557C
Sequence 91, Application US/08454557C
Sequence 91, Application US/08454557C
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                        9319 ATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAGATGGAGACCATC 9378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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    Length 105;
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89.0%; Pred. No. 6.5e-07;
Live 0; Mismatches 9; Indels
                                              Indels
                                                                                                                                                                              9379 CTGCTTAACACGATGAAACCCCGTCTTACTAAAAATACAAAATA 9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY U.S.A.

21P: 2000-3934

COUNTER READBABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R:
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
TELEPAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LEEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 DASE PAIRS
                                                                                                                                                                                                                             45 CTGGCCAATATGGTGAAACCCTGTCTACTAAAAGATGTAAAAA 1
Query Match 0.3%; Score 76.2; DB 5; Best Local Similarity 82.9%; Pred. No. 7.3e-09; Matches 87; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-340-426D-91/c; Sequence 91, Application US/08340426D; Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9369 GGAGACCATCCTGCTTAACACG 9390
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Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-454-557C-91
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Patent No. 594888
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
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                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATIC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67.6; DB 4;
Pred. No. 6.5e-07;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0609.3840002
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9369 GGAGACCATCCTGCTTAACACG 9390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CGACACCAGCCTGATGAACATG 2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis-
COMPUTER: IBM Pro-
OPERATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.0<sup>3</sup>
Matches 73; Conservative
                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                    RY: U.S.A.
20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      both
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US-08-450-673C-91/c
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both
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; TOPOLOGY: } PCT-US95-17111A-91
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US-08-454-557C-69
                                                                                                 Query Match
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Sequence 91, Application PC/TUS9517111A

Sequence 91, Application PC/TUS9517111A

Sequence 91, Application PC/TUS9517111A

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67.6; DB 4; Length 84;
Pred. No. 6.5e-07;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 20005-3934

COUNTER READABLE FORM:

MEDIUM TYPE: FILING DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/17111A

FILING DATE:
              APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CILLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
FELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9369 GGAGACCATCCTGCTTAACACG 9390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 CGACACCAGCCTGATGAACATG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%;
Best Local Similarity 89.0%;
Matches 73; Conservative
  CURRENT APPLICATION DATA:
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     both
                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-450-673C-91
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Sequence 69, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 10842 ACCATGCCCGCTAATTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGG 10901
                                                                            1 ACCACGCCCGCTAATTTTTTTTTTAGTAGACAGGGTTTCACCGTGTTGGCCAGG 60
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  Length 84;
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                                      9: Indels
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY 1995
CLASSIFICATION: 514
0.2%; Score 67.6; DB 6;
89.0%; Pred. No. 6.5e-07;
tive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2%; Score 62.8; DB 3; Best Local Similarity 97.0%; Pred. No. 8.1e-06; Matches 64; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36, 203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                       9369 GGAGACCATCCTGCTTAACACG 9390
                                                                                                                                                                           23 CGACACCAGCCTGATGAACATG 2
                    Best Local Similarity 89.09
Matches 73; Conservative
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Search completed: June 19, 2000, 03:08:43 Job time: 396853 sec

us-08-852-495c-2\_copy\_84000\_113000.rni

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                                                                                                                                             June 19, 2000, 03:02:32; Search time 17971 Seconds (without alignments) -1569.860 Million cell updates/sec
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1 TGTACTCTGGCTACCCTCTG........CTATAAACTGGAAACAACCC 29001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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1: 9b_bal:*

3: 9b_bal:*

4: 9b_ow:*

5: 9b_pal:*

7: 9b_pl:*

7: 9b_pl:*

10: 9b_pl:*

10: 9b_pl:*

11: 9b_pr:*

11: 9b_pr:*

13: 9b_pr:*

14: 9b_pr:*

13: 9b_pr:*

14: 9b_pr:*

13: 9b_pr:*

14: 9b_pr:*

13: 9b_pr:*

14: 9b_pr:*

14: 9b_pr:*

15: em_fun:*

16: 9b_vi:*

16: 9b_vi:*

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18: em_lum::*

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gb_htg4:*
gb_htg5:*
gb_htg6:*
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Maximum DB seq length: 110
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Perfect score:
Sequence:
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gb_p13:*
gb_pr5:*
gb_htg8:*
gb_htg10:*
gb_htg11:*
gb_htg11:*
gb_htg11:*
gb_htg14:*
gb_htg7:*
em_htg1:*
em_htg2:*
em_htg3:*
em_htg3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Searched:

Run on:

Description	05250 Human	X05249 Human LDL-r	1 Human	0	Human c	Human	3 Human	Human	Human c	Human	Human	X5//89 Human seque	Time in	. =	T de E	HILLIAN S	ל מפשוון	٠.	Human	Нишап	8 Human	Human S	_	HRX (1		5 WIAF-2393	Human	Human	Y.		H.Saplens	645550 WIAE-2595-5 W2612E Human alaha	dulian.	•		нашап	нишаи	Ξ		5 H.sap	Human	3555 Human	M14180 Human low d
a a		_		0 HSLDLRN2	Ξ		1 HSU67803	HUMALCE162	Ξ			3 HSBICBR	200000000000000000000000000000000000000	2	HIMPIDO3MS	HSTIFTBOR	HIMIDLEA	HSU67807	HSU67804	3 HUMUT7692A	0 HSLDLI12		3 G32614		1 HSU67806		HUMLDLRFL	3 HUMUT8164A	5/3203		O HESTHPAIB	UTIMODERA UTIMODERA	-	:	TOWN TOWN	HUMGALNSA	HUMGALNSA	Ξ		0 HSLAS27	HUMALCE4 3	HUMLDLRFL	HUMLDLRA2
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Score	99	89.4	89.4	9	2	83.2	82.6	81.2	79.8		٠.	0/2/		7. 47	7.4.2	74.47	73.6	73.4	71.4	70.8	70.8		0	69.8	9,69	69.4	69	69.2	4.80	7.69	0.0	60 67	- u				7.99	65.2	04.4	64.6	04.4	9	64
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ALIGNMENTS

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DEFINITION

**HSLDLRN2** 

RESULT

ACCESSION

VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

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*source: hypercholesterol aemia see sequence See X05248 for corresponding normal gene sequence In the defective LDL-receptor gene the deletion ocurred between two allu repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williamson, R. and Humphries, S. Unequelliamson, R. and Humphries, S. Unequel crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="blood leukocytes from a patient with familial" 1. 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSLDLRD2 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor mutated gene with intron 14 deletion junction.
                                                                                                                                                                                                                                                                                                                                                                    HSLDLRD1 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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                                                                                                   QY 22252 TTTTCTGAGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAATGCAGTGGCACAATCTCGGC 22311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="deletion junction region intron 12/ intron 15" 40 \ c \ 20 \ g \ t
                                                                                                                                   107 TITITIGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 ACAAAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCGGGAGGTGAG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Figure 3. Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Balsisegel, U., Dunning, A., Havinga, J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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Alu repetitive sequence; low density lipoprotein receptor.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alu repetitive sequence; low density lipoprotein receptor
  Length 107;

        QY
        27583
        GCAAGAGATTGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGA
        27629

        DD
        48
        GCAGGAAAATGGTTTGAACCCAGGAGGCAGAGGTTGTGGTGGTGAGGCGA
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
                                                                                                                                                                                                              QY 22312 TCACTGCAACCTCCGCCTCCCGGATTCACGCCATTCTCCTGCC 22354
                                                                                                                                                                                                                                      47 TCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTTCTGCC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%; Score 89.4; DB 10;
illarity 89.7%; Pred. No. 4.6e-06;
Conservative 0; Mismatches 11;
Score 90.2; DB 9;
Pred. No. 3.3e-06;
0; Mismatches 8;
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/db_xref="taxon:9606"
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  0.3%;
92.2%;
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                          Best Local Similarity 92.2
Matches 95; Conservative
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Best Local Similarity
Matches 96; Conserv
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HSLDLRD1/c
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HSLDLRD2
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                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 108)

1 (Bases 1 to 108)

Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for Eur.

Eur. J. Blochem. 164 (1), 77-81 (1987)
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1 (bases 1 to 107)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27523 ACAAAAATCAGCCAGGCGTGGTGGCATGTGCCTGTAATCCCAGGTACTCAGGAGGCTGAG 27582
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
                                                                                20-MAY-1992
                                                                                                                                                           X05250.1 GI:34337
Alu repetitive sequence; low density lipoprotein receptor
                                                                             HSLDLRN2 108 bp DNA PRI 20-MAY.
Human LDL-receptor gene intron 14 fragment (normal gene)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; DB 10; Length 108;
Pred. No. 1e-07;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY 27583 GCAAGAGATTGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGA 27629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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23 c 39 g 18 t
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30 c 35 g 1

    107
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/db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="embryo"
/sex="male"
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87161901
                                                                                                                                                                                                                human.
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source

FEATURES

COMMENT

JOURNAL MEDLINE intron

BASE COUNT

ORIGIN

HUMALCE162/c

g

8

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

TITLE

source

JOURNAL

FEATURES

BASE COUNT ORIGIN

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Indels

Length 108;

Gaps

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REFERENCE AUTHORS MEDLINE

COMMENT

JOURNAL

TITLE

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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Millianson, R. and Humphries, S.
Willianson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia 87161901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Moi. Biol. (1992) In press
Location/Qualifiers
                                             22306 CTCGGCTCACTGCAACCTCCGCCTCCCGGATTCACGCCATTCTCCTGCCTCAACCTCCCG 22365
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                                                                       108 CTCGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCG 49
                                                                                                                                                                                                                                                                              HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87895
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
                                                                                                                                    22366 AGTAGCTGGACCACAGGCGCCCGCCACCCCCAGCTAATTTT 22411
  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebra
Euthezia, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2.3e-05;
0; Mismatches 11;
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  0; Mismatches
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 g 18
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/sex="male"
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  94; Conservative
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es 92; Conserv
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                                                                                                                                                                                             Seource: hypercholesterol aemia
See XO5250 for corresponding normal gene sequence
In the defective LDL receptor gene the deletion ocurred between two
all repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
  1 (bases 1 to 1089).
Horsthamke,B., Belsiegel,U., Dunning,A., Havinga,J.R., Williamson,R. and Humphries,S.
Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Biochem. 164 (1), 77-81 (1987)
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|/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Alu repetitive sequence; low density lipoprotein receptor.
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 4.6e-06;
0; Mismatches 11
Primates; Catarrhini; Hominidae; Homo.
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23 c 39 g 18 t
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/db_xref="taxon:9606"
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DEFINITION

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Length 103;

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BASE COUNT ORIGIN

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FEATURES

MEDLINE

COMMENT

JOURNAL

20-MAY-1992

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Jases 1 to 107)
Sinnett,D., Richer.C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

1 (bases 1 to 103)

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences

J. Mol. Biol. (1992) In press

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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M87896
                                                                                                                                                                                         Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UURCE Homo sapiens male embryo carcinoma cDNA to other RNA ORGANISM' Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 GCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="carcinoma"
30 c 35 g 14
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/db_xref="taxon:9606"
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/sex="male"
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Best Local Similarity 87.3%;
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                27526 AAAATCAGCCAGGCGTGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCA 27585
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin!; Hominidae; Homo.
1 (bases 1 to 108)
Shaikh,T.H., Roy,A.M., Kim,J., Batzer,M.A. and Deininger,P.L.
CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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                                                                                                                                                                                                                                                               Score 83.2; DB 10; Length 108;
Pred. No. 5.4e-05;
0; Mismatches 13; Indels 0
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Pred. No. 6.9e-05;
0; Mismatches 9; Indels C
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
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see X05249 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GGAAAATGGTTTGAACCCAGGAGGCAGAGGTTGTGTGTTGAGGCGA 2
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Human small cytoplasmic Alu transcript.
U67803
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97415756
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                                                       1. .108
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/rpt_type=dispersed
39 c 30 g
                                                                                                                complement(<1. .65 /note="Alu repeat"
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/note="scAlu"
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nilarity 90.7%;
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ilarity 87.5%;
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HSU67803/c
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Indels

Length 107;

Score 81.2; DB 9; Pred. No. 0.00012;

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Aldridge, F.L.
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor mutated gene with intron 14 deletion junction.
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m c} 20 g 28~{
m t}
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                                                                                                               103 CTGGAGTGCAATGGCACGATCTCGGCTCACTGCAACCTCCGGCTTCCAGGGAT 44
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Primates; Catarrhini; Hominidae; Homo.
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Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 108)
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Qy 22367 GTAGCTGGGACCACAGGCGCCCGCCACCACGCCCAGCTAATTTT 22411
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                    Best Local Similarity
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*source: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
all-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
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/db_xref=-taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
/note="intron XIV fragment"
2. ... 40 g 20 t
                        Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Biochem. 164 (1), 77-81 (1987)
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Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler, R., Riley, J.H., Ogilvie, D.J., Anand, R., Buxton, J.,
Davies, J., Johnson, K. and Markham, A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
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Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 103)
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Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.
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Human sequence tagged site BICBR DNA from 19q13.
X57789
                                                                                                                                                                                                                                                                                                                of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 79.4; DB 10;
Pred. No. 0.00025;
0; Mismatches 16;
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91367697
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/clone="8IC8"
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/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 84.8%;
Matches 89; Conservative C
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from 19q13
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Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
                                                          Gaps
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAS derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-1991
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Query Match 0.3%; Score 76; DB 13; Length 103; Best Local Similarity 84.2%; Pred. No. 0.00096; Matches 85; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 110)
Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
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Human sequence tagged site BICOR DNA from 19q13.
X57789
                                                                                                                 QY 15312 TGAGACCAGCCAACATGGTGAAACCTCATCTTAGT 15352 | HIIII | HIIIIIIII | HIIIIII | Db 42 CTTGACCAGCCTGGCCAACATGGTGAAACCCTATCTACT 2
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Human small cytoplasmic Alu transcript.
U67807
U67807.1 GI:2289921
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97415756
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/clone="TscAlu6"
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/rpt_type=dispersed
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STS: myotonic dystrophy.
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/note="scAlu"
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                                                                                                                         Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals, Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler,R., Riley,J.H., Ogllvie,D.J., Anand,R., Buxton,J.,
Davies,J., Johnson,K. and Markham,A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12497 TAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATC 12556
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
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Pred. No. 0.0013;
0; Mismatches 14;
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/clone_lib="YAC library: ICI"
/clone="8IC8"
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/db_xref="taxon:9606"
/chromosome="19q13"
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Location/Qualifiers
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Job time: 427793 sec
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Best Local Similarity 85.6%;
Matches 83; Conservative
                                                                         Aldridge, F.L.
Direct Submission
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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29001
1 TGTACTCTGGCTACCCTCTG......CTA
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1007 1007 999 1099 1100 999 848	standard; DNA; 108 BP 1999 (first entry) phism: biallelic polymorphic phism: biallelic; hum on; phenotypic typing une disease; cancer; nt; marker; ss. 1997; 020313. 1997; 020313. 1996; US-30455. WHITEHEAD INST BIOME T, Lander ES, Wang D; 1966; US-30455. WHITEHEAD INST BIOME T, Lander ES, Wang D; 1966; US-30455. WHITEHEAD INST BIOME T, Lander ES, Wang D; 1966; US-30455. WHITEHEAD INST BIOME T, Lander ES, Wang D; 1966; US-30455. WHITEHEAD INST BIOME T, Lander ES, Wang D; 1966; US-30455. WHITEHEAD INST BIOME TO And Clear T, Lander ES, Wang D; 1966; US-30455. WHITEHEAD INST BIOME TO And Clear T, Lander ES, Wang D; 1966; US-30455. WHICH have been isolated not determining poly Trensics, paternity wiskort; Olesterolemia, polycy; trensics, von Willebran Theretion by pathoge Therefore treatme: Therapeutic
0000000000	5. standard; Di 15.; R-1999 (firs 12.1999 (firs 13.1999 (firs
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330 330 34 44 44 30 30 30 30 30 30 30 30 30 30 40 40 40 40 40 40 40 40 40 40 40 40 40	SULT X120, X102, X
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  resting or phenotypic typing for disease

claim 1, Page 219; 310pp; English.

Testing or phenotypic typing for disease

claim 1, Page 219; 310pp; English.

X10269-X12937 are human DMA fragments which contain biallelic polymorphic typing for disease

X10261-X12937 are human DMA fragments which contain biallelic polymorphic and the subject of the subj
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                                                               30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Polymorphism: biallelic; human; forensic; paternity testing; disease; detection; benotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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Human gene signature HUMGS07131.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
WQ9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid segments from the human genome - used for
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
HUGSON T, Lander ES, Wang D;
WPI; 98-286974/25.
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                                         X12095 standard; DNA; 108 BP.
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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WO9820165-A2.
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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences could be stranded DNA) which comprises one of the 7837 "GS" sequences user obtained from 3'-directed cDNA libraries prepared sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end ranslated sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs. In the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 34 A; 26 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27591 ATTGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAAATCGCGCCCACTGCACTCCAG 27650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                 Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ATCGCCTGAGCCCATGAGCCCAAGGCTGCAGTGAGCCATGGTCACGCCACTGNATTCCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 CCTGAGTGACAGAGCCCTGTTGAAACAACAACAACAACAAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T24892 standard; cDNA to mRNA; 100 BP
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Human gene signature HUMGS06998.
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Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09514772-A1.
01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okubo K;
Okubo K;
                        WPI; 95-206931/27.
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A single-stranded DNA for its complementary strand or the corresp.

Couble-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNA hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22247 TTTCTTTTTCTGAGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAATGCAGTGGCACAATC 22306
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WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.307-NOV-1996 (first entry)
Human gene signature HUMGS07131.
Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                              Human gene signature HUMCS06998.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59.2; DB 1;
Pred. No. 0.36;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 TCAGCTNATTGCAAATTCTGCCTCCCAGGTTCAAGCGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 G;
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T25009 standard; cDNA to mRNA; 108 BP.
T25009;
                                             T24892 standard; cDNA to mRNA; 100 BP.
T24892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1720; 2245pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 73,...
Local Similarity 73,...
T3; Conservative
                                                                                             05-NOV-1996 (first entry)
                                                                                                                                                                                                                                                              01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21451 TTATTTTTTTTTTGAGTCAGAGTCACACTCTGTCGCCCAGGCTGGAGTGCAGTGCGTGA 21510
                                                                                                                                                                                                                                          27591 ATTGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAAATCGCGCCCACTGCACTCCAG 27650
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                       2 ATCGCTTGAACCTGGGAGGCAGAATTTGCAATNAGCTGAGATTGCACCNTTGCACTCCNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1996 (first entry)
Human gene signature HUMGS08452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
HOMO saplens.
                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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0
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                    sequences) as a means of diagnosing abnormal cell function or recognising different cell types. Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
  СS
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                                                                                                                                          Length 100;
determined (esp. using primers and probes derived from the
                                                                                                                                                                                          25; Indels
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                                                                                                                                                                                                                                                                                                                                                                  62 CCTGGGTGACAGAGTGACACTCTGTTTGAAACAAACAAA 100
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                                                                                                                                               DB 1;
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                                                                                                                                            Score 60.8;
Pred. No. 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T26213/c
ID T26213 standard; cDNA to mRNA; 103
                                                                                                                                          Ouery Match 0.2%;
Best Local Similarity 74.7%;
Matches 74; Conservative
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Best Local Similarity 76.3%,
--hoq 74; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsubara K, Okubo K;
WPI; 95-206931/27.
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0; Gaps

Length 100;

22 T;

13 T;

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21

35 A;

87 BP;

Sequence

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                                                                                         A single-stranded DNA, which complementary strand or the corresp.

C double-stranded DNA, which comprises one of the 7837 "GS" sequences

C given in T19001-T26837 and which is able to hybridise to part of

the man genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

sequences were obtained from 3'-directed cDNA was intilated from the

C from various human tissues; synthesis of cDNA was intilated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

untranslated sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

c all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

c is constructed as oa st or reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

cetermined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for

crecognising different cell types.

Sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 914; 2245pp; Japanese.

C A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22239 TTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAATGCAGTG 22298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Human gene signature HUMGSO2944.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
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diagnosis of abnormal cell function, by preparing cDNA that
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                       reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGTGACCATGGCTCACTGCACCTTGGCCTCATGGGCTCAGGCGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%; Score 58.6; DB ilarity 71.0%; Pred. No. 0.45; Conservative 0; Mismatches
                                                                       Claim 1; Page 1748; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T21566 standard; cDNA to mRNA; 87 BP
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 76; Conserv
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WPI; 95-206931/27
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WO9514772-Al.
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                                                   tissues
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T21566
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Claim 1: Page 914: 2245pp; Japanese.

Claim 1: Page 914: 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

C double-stranded DNA) which comprises one of the 7817 "Gs" sequences

Given in T19001-T26837 and which is able to hybridise to part of

C flow arious DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

C from various human tissues; synthesis of cDNA libraries prepared

C from various human tissues; synthesis of cDNA libraries prepared

C 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

C untranslated sequence is unique to a particular mRNA species, almost

C all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

CC different mRNAs in the particular tissue from which it was derived.

CC determined (esp. using primers and probes derived from the GS

C sequences) as a means of diagnosing abnormal cell function or for

S Sequence 87 BP; 35 A; 21 C; 16 G; 13 T;
                                                                     23100 GATCACTTGAGTCCAGGAGTTTGAGACCAGCCTGGTCAACATGGCGAAACCTCATCTCTA 23159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9689 CCTGGCTAATTTTTGTATTTTAGGAGAGATGGGGTTTCACCATGTTGGCCAGACTGGTC 9748
                                     Gaps
                                                                                       WPI: 95-206931,27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                               03-AUG-1996 (first entry)

Human gene signature HUMGS02944.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;

human; cloning; mapphng; non-biased library; diagnosis; detection;

cell typing; abnormal cell function; ss.
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0.55;
 Length 87;
                                     17; Indels
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   DB 1;
                 0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 58; DB 79.8%; Pred. No. 0.55
                                   0; Mismatches
 Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                            T21566 standard; cDNA to mRNA; 87 BP.
T21566;
                                                                                                                                         Qy 23160 CAAAAATAAAAATTTGTCAGG 23183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T26828
ID T26828 standard; cDNA to mRNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9749 TCAAACTCCTGGCCTCAAGTGATC 9772
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0.2%;
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Watches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUBY) OKUBO K.
MALSUDATA K, Okubo K;
                                   67; Conservative
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T28837 and which is able to hybridise to part of human genomic DNA, cDNA orm RNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human biallelic polymorphic DNA fragment EST98276a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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Hudson T, Lander ES, Wang D;
WHI 98-286974/25.
New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
Claim 1; Page 219; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . e.g
                                                           Human gene signature HUMGS09078.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection;
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Sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           met. 23-200351/2/.
Identifying gene signatures in 3'-directed human cDNA library
for diagnosis of abnormal cell function, by preparing cDNA tha
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                                                                                                                                                             cell typing; abnormal cell function; ss.
Homo sapiens.
W09514772-Al.
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X12087/c

ID X12087 standard; DNA; 100 BP. AC X12087;
DT 30-MAR-1999 (first entry)
DE Human biallelic polymorphic DNA
W Polymorphism; biallellic; human; KW detection; phenotypic typing; cl
KW treatment; marker; ss. GS Homo saplens.
PN HOMO saplens.
PN WO982016-A2.
PP 14-MAY-1996; UZ0313.
PR 05-NOV-1996; UZ0313.
PR 06-NOV-1996; US-030455.
PT Hudson T, Lander ES, Wang D;
DR WPI: 98-286974/755.
PT Hudson T, Lander ES, Wang D;
DR WPI: 98-286974/755.
PT Geterming polymorphic forms for testing or phenotypic typing for testing or phenotypic typing for presenting or phenotypic typing for testing or phenotypic typing for the page 219; 310pp; Englise
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                                  (first entry)
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Okubo K;
                                                                                                                                                                                                                                                                                                                                                                    (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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                                  14-NOV-1996
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Best Local S
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PF 05-NOV-1997; U20313.

PR 06-NOV-1996; U20-3045.

PR 06-NOV-1996; U20-30465.

PR 06-NOV-1996; U20-30465.

PR (WHED ) WHITEREAD INST BIOMEDICAL RES.

PR Hudson T. Lander ES. Wang D;

DR WPI: 99 286974/25.

PR 1 Hudson T. Lander ES. Wang D;

DR WPI: 99 286974/25.

PR 1 Hudson T. Lander ES. Wang D;

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PR 4 1 Hudson T. Lander ES. Walleated To Wal
X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268 The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in c.g. forensies, paternity testing or for phenotypic typing for diseases such as agammiglobulinemia, diabetes insipidua, lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aidrich syndrome, Fabry's disease, familial spherocytosis, on Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectssia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous such autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microcypanisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, and see indurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human biallelic polymorphic DNA fragment EST98276c. Polymorphism, biallelic; human; forensic; paternity testing; disease; Polymorphism; biallelic; human; forensic; infection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament.
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ID X12085 standard; DNA; 100 BP. X12085; DT 30-MAR-1999 (first entry)

E Human biallelic polymorphic DNA Polymorphism; biallelic; human; W detection; phenotypic trying; ch autoimmune disease; cancer; infl treatment; marker; ss.

NW autoimmune disease; cancer; infl twanteatment; marker; ss.

HOMO sapiens.

PP WO9820165-A2.

PP 05-NOV-1996; US-030455.

PR (WHED) WHITENEAD INST BIOMEDICA PT detering on phenotypic trying for testing or phenotypic trying polymorphic CC x09121-X10268. The base occupying complete or determining polymorphic claudiscapering cc such as agammaglobulinemia, diabor muscular dystrophy, Wiskott-Aldra muscular dystrophy, Wiskott-Aldra CS such as agammaglobulinemia, polycystic claudiscapering cc syndrome, osteogenesis imperfect cc syndrome, fertility, appearance (e.g. bc endurance, fertility, and susceptoreasts)
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Matches 72; Conservative
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RESULT 14

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                                                                                                                                                                                             GTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCCAAGGTAAGCAGATCACTTGAGGT 27467
     polymorphic nucleic acid
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drugs or therapeutic treatments. The isolated polymorphic nucleic acis segments can also be used to produce medicaments for the treatment or
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                                                                                                                                                                                                                                   99 GTGACTCACACCTATAATCCTGGCACTTTRGGAGGCTTAGGAAGGAGGAGTTGTTTGAAAC 40
                                                                                                                                                                                                                                                                                                                                                                                 44-JUL-1996 (first entry)
Human gene signature HUMGS02180.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
HOMO Saplens.
W09514772-A1.
01-JUN-10-6
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Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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                                                                                                                 DB 1; Length 100;
0.8;
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                                                           30 T;
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                                                                                                                   Score 57; DB 1; Pred. No. 0.8; 1; Mismatches
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                                       prophylaxis of such diseases.
Sequence 100 BP; 22 A;
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Best Local Similarity 72...
Best Local Similarity 72...
72, Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATE,) MATSUBARA K.
(OKUB/) OKUBO K.
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                                                             Sequence
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The Wew isolated nucleate actus segments. Item the number yencer testing or phenotypic typing for disease

T determining polymorphic forms for use in e.g. forensics, paternity

T testing or phenotypic typing for disease

PS Claim 1: Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

CX 09121-X10268 The base occupying the polymorphic site is indicated by

CX 09121-X10268 The base occupying the polymorphic site is indicated by

CX of appropriate IUPAC-IUB ambiguity code. These fragments can be used in

CX of a propriate IUPAC-IUB ambiguity code. These fragments can be used in

CX of a forensics, paternity testing or for phenotypic typing for diseases

CX ouch as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,

CX of a gammaglobulinemia, familial colonic polyposis, Enlers-Danios

CX of a procytosis, von Willebrand's disease, hereditary

CX syndrome, osteogenesis imperfects, acute intermittent porphyria,

CX syndrome, fertility, and susceptibility or receptivity to particular

CX concert can also be used to produce medicaments for the treatment or

CX syndromes of such account of produce medicaments or have a mean or account or a
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Human biallelic polymorphic DNA fragment EST98276b.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                           Human biallelic polymorphic DNA fragment EST98276a.
Polymorphism, biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; detection; phenotypic typing; characteristic; infection; hereditary; dutolimmune disease; cancer; inflammation; drug; therapy; medicament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid segments from the human genome - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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(WHED) WHITEMEAD INST BIOMEDICAL RES.
HUGSON T, Lander ES, Wang D;
WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 C;
                        X12087 standard; DNA; 100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X12086 standard; DNA; 100 BP
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Best Local Similarity 75.0%;
Matches 69; Conservative
                                                                      30-MAR-1999 (first entry)
                                                                                                                                                                                                       treatment; marker; ss.
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WO9820165-A2.
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Provided to the following by the following for disease in e.g. forensics, paternity testing or phenotypic typing for disease by testing or phenotypic typing for disease contain it page 219; 310pp; English.

Claim 1; Page 219; 310pp; English.

Contain 1; Page 219; 310pp; English.

Contain 2; Page 219; 310pp; English.

Contain 3; Page 219; 310pp; English.

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Contain 3; Page 219; 310pp; English.

Contain 4; Pabry 4; Page 4; Pabry 5; P
Hudson T, Lander ES, Wang D;
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ö 0; Gaps Query Match 0.2%; Score 56.4; DB 1; Length 100; Best Local Similarity 75.0%; Pred. No. 0.99; Matches 69; Conservative 1; Mismatches 22; Indels ð 셤

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Search completed: June 19, 2000, 11:47:50 Job time: 427781 sec

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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                        June 18, 2000, 22:02:37; Search time 8514.75 Seconds (without alignments) 13805.165 Million cell updates/sec
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29001
1 TGTACTCTGGCTACCCTCTG.......CTATAAACTGGAAACAACCC 29001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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MO 63108

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1. .106
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:1140858"
/clone="IMAGE:1140858"
/clone="lib="Stratagene hNT neuron (#937233)"
/dac_stage="hMT neurons"
/dab_host="Solk (Ranamycin resistant)"
/note="Vector: pBluescript SK; Site_1: EcoR; Site_2:
Xhoi; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; UnizAAP XR Vector; -5' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT 3'
CTCGAGTTTTTTTTTTTTTTTT 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA243009 109 bp mRNA EST 11-MAR-1998 zr25h02.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens CDNA clone IMAGE:664467 3' similar to contains Alu repetitive element; contains element LTR1 repetitive element; , mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Lebnon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NII.
                                                                                                                                                                                                                                                                                                                                                                                         22416 TITITAGTAGAGACAGGGTTTCACCGTGTTAGCCGGGATGGTCTCGATCTCCTGACCTCA 22475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Fils cine is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
                                                      Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ;
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     1 ITITIAGTAGAGACGAGGTITCACCGTGTIAGCCAGGATGGTCTCGATCGTCCTGACCTCG 60
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                                                                                                                                                                                                                                                                                                                                          DB 37; Length 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                      0.3%; Score 93.2; DB
92.5%; Pred. No. 0.15;
live 0; Mismatches
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AA243009.1 GI:1873869
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Matches 98; Conserv
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AUTHORS
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AA243009
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A0321855 RPCI11-11
AA520812 2506a05.s
AA812141 ob48h02.s
A700000 tt36a10.x
AA78093 7H12D08 C
AA078003 7H12D08 C
                                                                                                                                                                                                                                                                                                   A0535244 RPCI-11-3
A1991750 W448e01.x
A1991750 W448e01.x
B17434 345K2.TVB C
A035334 RPCI-11-S
A0321855 RPCIII-11
B17434 345K2.TVB C
                                                                    AA855205 ak64h01.s
AA244245 nc07a04.s
AA381369 EST94442
B65160 CIT-HSP-201
AA64562 nt75f10.s
                    AA703692 ag81a10.r
AA243009 zr25h02.s
AA250812 zs06a05.s
B48914 RPCII1-4A12
                                                                                                                               AA565533 nK42b11.s
AA828124 od71a07.s
AQ003188 RPC111-1D
AA654562 nt75f10.s
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AQ028649 CIT-HSP-2
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AQ535244 RPCI-11-3
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AQ240182 CIT-HSP-2
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AQ637292 RPCI-11-4
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AA244245 nc07a04.s
AA897366 am06h02.s
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AA807640 nx08b05.s
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AQ076649 CIT-HSP-2
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1981a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases i to 106)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397630.
 Description
                                                                                                                                                                                                                                           r94466
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AA250812
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AA835205
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AA703692.1 GI:2713610
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Query Match 0.3*
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Matches 94; Conservative
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                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:664467"
/clone="IMAGE:664467"
/clone="IMAGE:664467"
/clone="IMAGE:664467"
/clone="IMAGE:664467"
/clone="IMAGE:664467"
/tlssue_type="neuroepithelial cells"
/dev_stage="neuroepithelial cells"
/dev_stage="neuroepithelial cells"
/dev_stage="neuroepithelial cells"
/dev_stage="Ntera-" neuroepithelial cells"
/dev_stage="SOLR (kanamycin resistant)"
/dev_stage="Ntera-" solte-" (anamycin resistant)"
/dev_stage="Ntera-" (
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AA250812 GI:1885774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22413 GTATTTTTAGTAGAGACAGGGTTTCACCGTGTTAGCCGGGGATGGTCTCGATCTCCTGACC 22472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases to 106)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
On Sep 12, 1996 this sequence version replaced gi:1407356.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Fabril: Robert Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91.4; DB 30; Length 109;
Pred. No. 0.24;
0; Mismatches 11; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="germinal center B cell"
/lab_host="DH10B"
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/db_xref-"taxon:9606"
/clone-"IMAGE:684368"
                                                                  /organism="Homo sapiens"
/db_xref="GDB:5426481"
Location/Qualifiers
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Best Local Similarity 89.9
Matches 98; Conservative
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Eutheria: Primates; Catarrhini; Hominidae; Wertebrata; Mammalla; Eutheria: Primates; Catarrhini; Hominidae; Homo.

Solden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building

Unpublished (1997)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 80200

Fax: 40200

Fax: 4
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QY 12497 TAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATC 12556
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/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCIII "Human Male BAC Library"
1 28 c 30 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPCIII-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12, genomic survey sequence.
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Pred. No. 0.31;
0; Mismatches 6;
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/db_xref="GDB:7501163"
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/clone="RPCI-11-4A12"
/clone_lib="RPCI-11"
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22317 GCAACCTCCGCCTCCCGGATTCACGCCATTCTCCTGCCTCA 22357
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Library 27 9 24 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 101)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU.NCI human EST Project
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                                                                           22412 TGTATTTTAGTAGAGACAGGGTTTCACCGTGTTAGCCGGGATGGTCTCGATCTCCTGAC 22471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 TGTATTTTTAGTAGAGAGGGGTTTCACCGTTTTAGCCGGGATGGTCTCGATCTCTGAC 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Nov 29, 1993 this sequence version replaced g1:636191.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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0.3%; Score 88.6; DB 84; Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1412689"
/clone_lib="Barstead pancreas HPLRB1"
                                                                                                                                                                              Score 88.2; DB 39;
Pred. No. 0.56;
0; Mismatches 8;
                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult, 34 years"
/lab_host="DH108"
              Pred. No. 0.5;
                                   0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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92.1%;
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              91.38;
                                     94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Query Match
                     Local
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ORIGIN
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AUTHORS
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JOURNAL
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// note="Vector: pawp10; Site_1: Not1; Site_2: EccR1; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EccRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pawp10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman." I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI-GGAP Intp://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                      ncc7504.51 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Jan 24, 1995 this sequence version replaced gi:634306.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
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Pred. No. 0.54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"NCI_CGAP_Prl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1007406"
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Location/Qualifiers
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ilarity 87.3%;
Conservative (
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Best Local Similarity
Matches 96; Conserv
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Homo sapiens
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AA654562/c
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SOURCE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C., Cocayne, J.D., White, O., Sutton, G., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., T., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Otterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A., Kaymond, L., Wei Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Kaymond, L., Wei Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Frannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C., Praser; C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C., Only M. Schon, M. Straser, C.M. and Venter, J.C., Only M. Schon, M. Straser, C.M. and Venter, J.C., Only M. Schon, M. Sch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                     AA381369 101 bp mRNA EST 21-APR-1997 EST94442 Activated T-cells I Homo sapiens CDNA 5' end similar to EST containing Alu repeat, mRNA sequence.
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/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Sep 12, 1996 this sequence version replaced gi:1407448.
Other_ESTs: THC170052
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Nature 377 (6547 Suppl), 3-174 (1995)
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The Institute for Genomic Research
The Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Pred. No. 0.62;
0; Mismatches 9;
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/db_xref="ATCC (inhost):185728"
/db_xref="taxon:9606"
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Best Local Similarity 91.1%;
Matches 92; Conservative 0
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RESULT 7
AA381369/c
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clones are available from Research Genetics (info@resgen.com). BAC end search page:
end search page:
thtp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                     1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QY 27541 TGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAAGAATTGCTTGAA 27600
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B65160 108 bp DNA GSS 21-JUN-1998 CIT-HSP-2017G2.TRB CIT-HSP Homo sapiens genomic clone 2017G2, genomic survey sequence.
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Other_GSSs: CIT-HSP-2017G2.TFB
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
713: 301 838 0208
Fax: 301 838 0208
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/db_xref="taxon:9606"
/clone="2017G2"
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/cell_type="Sperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:2590716
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                          Tumor Gene Index
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Matches 94; Conserv
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                                                                                                     Tumor Gene Index
Dupublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393451.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Prayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"vector: paMP10; Site_1: Not1; Site_2: EcoRI; Ist Strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of FCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10?)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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0; Mismatches
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/clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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32 c
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CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbl.nlm.nlh.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                             Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                        CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 TGGTGTGTGCTGTGAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATCACTTGAACCT 48
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Unpublished (1997)
On Jan 17, 1998 this sequence version replaced g1:1899815.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393355.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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ilarity 87.9%; Pred. No. 0.9;
Conservative 0; Mismatches
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Seq primer: -40ml3 fwd.
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ilarity 87.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pAMP10; mRNA made from invasive ovarian tumor, CDNA made by oligo-dT priming. Non-directionally cloned Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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1 (bases 1 to 110)
Adams, M.D. Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
                                                              Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: middam@figr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@deJong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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RPCIII-1D10.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1D10,
genomic survey sequence.
AQ003188 GI:3030392
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                 cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome St Clone distribution: NCI-GGAP clone distribution in found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0200
                                                                                                                                                                   Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 93.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /clone-"IMAGE:1373364"
/clone_lib-"NCI_CGAP_Ov2"
/sex-"female"
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                               /tissue_type="ovary"
/lab_host="DH10B"
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Smmert-Buck, M.D., Ph.D.
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93; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bass 1 to 102)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

On Sep 12, 1996 this sequence version replaced gi:1393451.
On Sep 12, 1996 this sequence version replaced gi:1393451.
Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
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/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22408 TTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTTAGCCGGGATGGTCTCGATCTCC 22467
                                                                                                                                                                                                                 /seal_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Wector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
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Pred. No. 0.81;
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/db_xref="taxon:9606"
/clone="IMAGE:1204363"
                                                                 sapiens
                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-1D10"
/clone_lib="RPCI-11"
                                                                                  /db_xref-"GDB:7500081
Location/Qualifiers
                             1. .110
/organism-"Homo
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Indels

11;

Length 103;

18-MAY-1999

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22288 GGAATGCAGTGGCACAATCTCGGCTCACTGCAACCTCCGCCTCCCGGATTCACGCCATTC 22347
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                                                                                                                                                                                                                                                                                                                                                                    AQ535244 103 bp DNA GSS 18.
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
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                                                                                                                                                                                                                                              61 TCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGACGCCTGC 103
                                                       Score 86; DB 108;
Pred. No. 0.97;
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          histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman.
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1 (bases 1 to 103)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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Clones are derived from the human BAC library RPCI-11. For BAC
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On Feb 19, 1999 this sequence version replaced gl:4146076.
Other_GSSs: RPCI-11-451A15.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
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RPCI-11-451A15.TJ RPCI-11 Homo sapiens genomic clone
RPCI-11-451A15, genomic survey sequence.
                                                                                                                                                                                                                                                               DB 36; Length 102; 0.97;
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Tel: 301 838 0200
Fax: 301 838 0208
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong mac.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (lnfo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: T7
Class: BAC ends.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

2 hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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/note="type="Lymphocytes"
/note="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Pred. No. 1.1;
0; Mismatches 11; Indels
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/organism="Homo sapiens"
/db_xref="GDB:7621533"
/db_xref="taxon:9606"
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/clone_11b="RPCI-11"
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Db 43 TGACCTCAAGTGATCTGCCCGTCTTGGCCTCCCAAAGTGCTGG 1

Search completed: June 19, 2000, 06:28:49 Job time: 409896 sec

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEDATIN Release #1.0, Version #1.30 (EPO)
CURRETA APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78.4; DB 4;
Pred. No. 2.4e-08;
US-08-340-426D-92
US-08-450-73C-92
US-08-454-557C-91
US-08-454-657C-91
US-08-450-673C-91
US-08-450-673C-91
US-08-454-557C-57
US-08-454-557C-69
US-08-454-557C-69
US-08-454-557C-69
US-08-454-557C-69
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-60
US-08-450-673C-60
US-08-44-557C-60
US-08-44-557C-60
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TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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FILING DATE: US-JUN-1995
CIASSIPECATION: 124
PRICATION: 124
PRICATION: 124
PRICATION: 124
PRICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTONEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DCCKET NUMBER: D-0021.3E
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 65, Application US/08481658B Patent No. 5955075
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Best Local Similarity
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US-08-481-658B-65
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1 TGTACTCTGGCTACCCTCTG..........CTATAAACTGGAAACAACC 29001
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-486-756A-65
US-08-486-756A-65
US-08-487-739-65
US-08-487-504A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-787-739-65
US-08-787-739-65
US-08-786-736-70
US-08-454-557C-70
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US-08-454-557C-70
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US-08-450-673C-70
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US-08-340-426D-69
US-08-450-673C-69
PCT-US95-17111A-69
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US-08-340-426D-91
US-08-450-673C-91
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 110
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US-08-486-756A-65
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Gaps
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SOFTWARE: PETENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRICA PRICA PRICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
RAME: LAUGH, LOOP INFORMATION:
REFERENCE/DOCKET NUMBER: 0-0021.3D
TELECHMONICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Indels
0; Mismatches 16; Indels
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Pred. No. 2.4e-08;
0; Mismatches 16
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94920
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              US-08-477-504A-65
Sequence 65, Application US/08477504A
Patent No. 5972353
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.3%;
84.6%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.3
Best Local Similarity 84.6
Matches 88; Conservative
88; Conservative
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US-08-477-504A-65
Matches
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21613 TTTTTGTATTTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTCCAACTCC 21672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78.4; DB 4; Length 105;
Pred. No. 2.4e-08;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21673 TGACCTCATGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGAT 21716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                 APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF EXQUENCES: 86
ADDRESSE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-0021.3C
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Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET UNBER: D-C
TELECOMMUNICATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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STREET: 6 Mariposa Court
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                                                                                                                                                                                                                             6 Mariposa Court
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.3
Best Local Similarity 84.6
Matches 88; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         California
: USA
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CITY: Tiburon
STATE: Califorr
COUNTRY: USA
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US-08-486-756A-65
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RESULT

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FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/485,049
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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Best Local Similarity 84.69
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-981-0332 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
APPLICATION NUMBER:
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                                                                                                                                                                                                           OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: US-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: US-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEBRANCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEBRANCE/DOCKET NUMBER: D-0021.3D
TELEBRANCE/DOCKET NUMBER: TOWNER: D-0021.3D
TELEBRANCE/DOCKET NUMBER: TOWNER: TELEBRANCE/DOCKET NUMBER: S-0021.3D
TELEBRANCE/DOCKET NUMBER: TELEBRANCE/DELEBRANCE/DELEBRANCE/DOCKET NUMBER: TELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DOCKET NUMBER: D-0021.3D
TELEBRANCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION TON SEG ID NO: 65:
SEQUENCE CHARACE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DELEBRANCE/DOCKET NUMBER: D-0021.3D
TELEBRANCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION TON SEG ID NO: 65:
SEQUENCE CHARACE/DELEBRANCE/DOCKET NUMBER: D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 21673 TGACCTCATGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGAT 21716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ATTLE OF INVENTION:
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
DORRESPONDENCE ADDRESS:
STREET: 369 Pine Street, Suite 610
                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
                        California
: USA
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Best Local Similarity
Matches 88; Conserv
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US-08-787-739-65
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                                                      COUNTRY:
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21613 TTTTTGTA,TTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTCCCAACTCC 21672
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Pred. No. 2.4e-08;
0; Mismatches 16;
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APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: GMatiposa Court
CITY: Tiburon
STATE: California
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-UNN-1995
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-UNN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-UNN-1995
ATTING DATE: 07-UNN-1995
ATTING DATE: US 08/487,077
FILING DATE: US 08/487,077
ATTING DATE: UNDMER: US 08/487,077
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NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION:
TELEPHONE: 415-435-2034
                                                     D-0021.3D
                         REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                     LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
           Lauder, Leona L.
                                                                                                                                                                                                                                                         TOPOLOGY: linear
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US-08-477-504A-65
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 GCCTGGCCAATATGGTGAAACCCTGTCTTACTAAAAGATGTAAAAA 2
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Best Local Similarity 84.0%; Pred. No. 4.3e-06;
Matches 89; Conservative 0; Mismatches 15,
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US-08-477-504A-65/C
S-08-477-504A-65/C
Sequence 65, Application US/08477504A
PREACH NO. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Gmariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                              NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/POCKET NUMBER: D-0021.3E
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPRAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 1D NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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US-08-481-658B-65
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QY 15260 ATACCAGCACTTTGGGAGGCCGATGTGGGTGGATCACCTGAGGTCAGGAGTTTGAGACCA 15319
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COMPUTER: INP PET COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
Query Match 0.2%; Score 68; DB 4; Length 105; Best Local Similarity 84.0%; Pred. No. 4.3e-06; Matches 89; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                              Qy 15320 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 15365
                                                                                                                                                                                                                                                                                 Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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us-08-852-495c-2\_copy\_112000\_141000.rni

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15260 ATACCAGCACTTTGGGAGGCCGATGTGGGTCACCTGAGGTCAGGAGTTTGAGACCA 15319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          RESULT 10
US-08-787-739-65/c
; Sequence 65, Application US/08787739
; Patent No. 6027887...
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TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415-981-0332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-08-787-739-65
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                                                                                                                                                                                                            15260 ATACCAGCACTTTGGGAGGCCGATGTGGGTGACATCACCTGAGGTCAGGAGTTTGAGACCA 15319
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                        0.2%; Score 68; DB 4; Length 105;
84.0%; Pred. No. 4.3e-06;
tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%; Score 68; DB 4; Length 105;
84.0%; Pred. No. 4.3e-06;
tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                QY 15320 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 15365
                                                                                                                                                                                                                                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-0021.3D
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US-08-485-862B-65/c
; Sequence 5, Application US/08485862B
; Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
; MOLECULE TYPE: DNA (genomic);
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-486-756A-65
                                                                                                                      Query Match 0.2%
Best Local Similarity 84.0%
Matches 89; Conservative
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Best Local Similarity 84.0
Matches 89; Conservative
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105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCAC--AAGGTCAGGAGTTTGAGAGCA 48
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/77,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
ANDE: TANGOR TANGOR TOWNEY TOWNEY
ANDER TANGOR TANG
                                                                                                                 Qy 15320 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 15365
                                                                                                                                                                       47 GCCTGGCCAATATGGTGAAACCCTGTCTTATATAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEGUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Leona L. Lauder
STREET: 369 pine Street, Suite 610
CITY: San Francisco
STATE: Callfornia
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                       Sequence 70, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                            15260 ATACCAGCACTTTGGGAGGCCGATGTGGGTGGATCACCTGAGGTCAGGAGTTTGAGACCA 15319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21598 ACCAAGCCCGGCTAATTTTTGTATTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGG 21657
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                                                                    Gaps
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85.9%; Pred. No. 0.00016;
tive 0; Mismatches 11; Indels
                     Length 105;
                                                                                                                                                                                                      QY 15320 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 15365
                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/45,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION : 314
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGESTRATION NUMBER: 36,203
REFERENCE/DOCKET 1020; 311-2600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPROME (202) 371-2600
                                                                                                                                                                                                                                                 47 GCCTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
                  0.2%; Score 68; DB 5; lilarity 84.0%; Pred. No. 4.3e-06; Conservative 0; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY 21658 CTGGTCTCCAACTCCTGA 21675
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                                          Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Wash
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US-08-454-557C-70
                                                                                                                                                                                                                                                                                                                                         US-08-454-557C-70
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                     Query Match
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Patent No. 5948688
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
APPLICANT: de la Monte, Suzanne
PEPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21598 ACCAAGCCCGGCTAATTTTTTTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGG 21657
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                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.2%; Score 60.4; DB 4; Best Local Similarity 85.9%; Pred. No. 0.00016; Matches 67; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0609.3840002
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
SOFTWANE: PatentIn Release.
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TELECOMMUTCATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR EGO ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OY 21658 CTGGTCTCCAACTCCTGA 21675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CTGGTGTCGAACTCCTGA 78
                                                                                   NUMBER OF SEQUENCES: 121 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    both
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Gaps

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Length 78;

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APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 21598 ACCAAGCCCGGCTAATTTTGTATTTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGG 21657
                                                                                                                                                                                                                                                                                                                              ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                11; Indels
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                                                                                                                                           Query Match
0.2%; Score 60.4; DB 6;
Best Local Similarity 85.9%; Pred. No. 0.00016;
Matches 67; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,203
REFERENCE/DOCKET UNDRER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 371-2600
TELEFRAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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US-08-454-557C-70/c
                                PCT-US95-17111A-70
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US-08-454-557C-70
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%; Score 60.4; DB 4; Length 78;
85.9%; Pred. No. 0.00016;
tive 0; Mismatches 11; Indels
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ZIP: 20005-3934
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                     APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 30-MAY-1995
TATORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 0609.3840004
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION TOWNORMATION:
TELEFORMUNICATION TOWNORMATION TOWNORMA
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 21658 CTGGTCTCCAACTCCTGA 21675
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Best Local Similarity 85.98
Matches 67; Conservative
CURRENT APPLICATION DATA:
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STRANDEDNESS: both
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PCT-US95-17111A-70
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US-08-450-673C-70
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Length 78;

Search completed: June 19, 2000, 11:34:48 Job time: 427218 sec

us-08-852-495c-2\_copy\_112000\_141000.rni

Run on:

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June 19, 2000, 11:28:29; Search time 17971.8 Seconds (without alignments) -1569.789 Million cell updates/sec
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29001
1 GGTTTTGACAAAGGTGTCAA......TCCTTCAGGAGTTACTTCTA 29001
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 882769 seqs, -486395729 residues
                                                                                                                                       - nucleic search, using sw model
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Listing first 45 summaries
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1: 9b_bal:*

3: 9b_om:*

4: 9b_om:*

5: 9b_pl:*

7: 9b_pl:*

7: 9b_pl:*

10: 9b_pr:*

10: 9b_pr:*

11: 9b_pr:*

11: 9b_pr:*

11: 9b_pr:*

12: 9b_pr:*

13: 9b_pr:*

14: 9b_pr:*

15: 9b_ron:*

16: 9b_ri:*

16: 9b_ri:*

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16: 9b_ri:*

17: em_hum:*

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18: em_on:*

18: em_on
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gb_htg4:*
gb_htg5:*
gb_htg6:*
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Maximum DB seq length: 110
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Perfect score:
Sequence:
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gb_htg7:* em_htg1:* em_htg3:*	htg hum	ם ם ם ם	gb_htg11:* gb_htg12:* gb_htg13:* gb_htg14:*
445:	4 4 8 : 50 :	51: 52: 53: 54:	55: 56: 57: 58:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Human	X05250 Human LDL-r	Нишап	Human	Human c	Human	Human	8	9 Human	Human	Human c	Human	Human	Нишап	/ Human smal		0	Human c	Human LDL	5 WIAF-	Human carc	Human 1	Human	fami	Human low c		5 A009L30 F	MI41/8 Human low d		L30176 Human STS U		Human	1 Humar	Нишап	5 WIAF-	≖	٦,	5 H.sapiens	99 Human STS	KU3555 Human Low d	-	-	2906 A009W09 Hu	G02323 human STS S
SUMMARIES	ΩI		HSLDLRN2	HUMALCE162	HUMALCE272	HUMALCE221	HSLDLRN2	HSU67804	HSU67808	HS8IC8R	HUMLDLRA1	HUMALCE162	HS8IC8R	HSLDLRD1	HSLDLRD2	HS067807	HUMUT8164A	879560		HSLDLI12		HUMALCE43	HUMLDLRA2	HSU67807	HUMLDLRDJ	HUMLDLRA2	HUMUT931A	G32655	HUMLDLKAI	HITMU 1 DO 3 M 5	HUMUT 8002B	HUMLDLRDJ	HSLDLRD1	HSLDLRD2	HUMLDLRM	G43535	HUMGALNSA	HSSTHPKIB	HSLAS27	HUMUT931A	HUMLDLRFL	5/9560	AKUSISZI	~ 4	602323
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KEYWORDS
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1 (bases 1 to 108)

Horst Lough.

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for Eur.

Eur. J. Blochem. 164 (1), 77-81 (1987)
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Shalkh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Shalkh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
1. .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26228 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAA 26287
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                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  01-AUG-1997
                                                                                                                                                                                   1 (bases 1 to 108)
Shaikh,T.H., Roy,A.M., Kim,J., Batzer,M.A. and Deininger,P.L.
CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Human LDL-receptor gene intron 14 fragment (normal gene).
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
1 Location/Qualifiers
1. .108
                                    PRI
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                   HSU67803 108 bp RNA
Human small cytoplasmic Alu transcript.
U67803
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
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AUTHORS
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QY 26334 AAAAATTAGCCAGGCATGGTAGCACATGCCTGTAATCCCAGCTACTCAAGAGGCTGAGGC 26393
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1 (bases 1 to 107)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                         Gaps
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Human carcinoma cell-derived Alu RNA transcript, clone CE272.
M87899
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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                                                                                                                                                                                                    Length 108;
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86.4%; Pred. No. 0.0047;
tive 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                               Score 85.2; DB 10;
Pred. No. 0.00098;
0; Mismatches 13;
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/organism="Homo sapiens"
/db.xref="taxon:9606"
1. .108
/note="intron XIV fragment"
23 c 39 g 18 t
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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30 c 35 a 14
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ilarity 87.7%;
Conservative C
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hes 93; Conserv
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Matches 89; Conserv
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source

JOURNAL

FEATURES

REFERENCE AUTHORS

TITLE

BASE COUNT ORIGIN

Matches

8

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Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Cartarhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Millamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
Eur. J. Biochem. 164 (1), 77-81 (1987)
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Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-40G-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy 13383 CTCAACTCACTGCAACCTCCACCTCGGATTCAGGCAATTCTCCTGCCTCAGCCTCCGG 13442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 CTCGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCG 49
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
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                                                                                                                                      Alu repetitive sequence; low density lipoprotein receptor.
                         Human LDL-receptor gene intron 14 fragment (normal gene)
X05250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy 13443 AGTAACTGCGACTACAGGTGCGCACCACCACAAGTGGCTAATTTTTT 13490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 0.013;
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Human small cytoplasmic Alu transcript.
U67804
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J. Mol. Biol. 271 (2), 222-234 (1997)
97415756
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23 c 39 g 18 t
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/db_xref="taxon:9606"
/clone="TscAlu3"
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/db_xref="taxon:9606"
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                                                                                                             GI:34337
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VERSION
KEYWORDS
SOURCE
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TITLE
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HSU67804
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1 (bases 1 to 104)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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1 (bases 1 to 103)
2 (all the control of the 
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Human carcinoma cell-derived Alu RNA transcript, clone CE221
M87896
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tive 0; Mismatches 13; Indels
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79.2; DB 9;
Pred. No. 0.0077;
0; Mismatches 13;
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                                                                                                                                                                                                     1. .104
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev.stage="embryo"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="carcinoma"
26 c 37 g 1
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 g 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 0.3%;
1 Similarity 87.0%;
87; Conservative
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Best Local
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DEFINITION ACCESSION VERSION

ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

BASE COUNT ORIGIN

Matches

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RESULT 5 HUMALCE221

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Gaps

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Indels

19;

Length 108;

01-AUG-1997

PRI

/rpt\_family="Alu"

RESULT 6
HSLDLRN2/c

BASE COUNT ORIGIN

Matches

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DEFINITION

RESULT HSU67808

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

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Analysis of the LDL-receptor gene of a patient with familial hypercholesterolemia (FH) revealed the deletion of exon 5 resulting from a homologous recombination between repetitive Alu sequences of intron 4 and intron 5.

Location/Qualifiers
                                                                                                                                          Direct Submission
Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler, R., Riley, J.H., Ogilvie, D.J., Anand, R., Buxton, J.,
Davies, J., Johnson, K. and Markham, A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97).

Hobbs, H.H., Brown, M.S., Goldstein, J.L. and Russell, D.W.

Deletion of exon encoding cysteine-rich repeat of low density impoprotein receptor alters its binding specificity in a subject with familial hypercholesterolemia

J. Biol. Chem. 261 (28), 13114-13120 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DY 13498 CTGTAGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTGAAGTG 13557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMLDLRA1 97 bp DNA PRI 07-JAN-1995 Human low density lipoprotein receptor gene, intron 4 (partial).
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 103)
Aldridge, F. L.
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                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 19 (17), 4787 (1991)
91367697
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/clone_lib="YAC library: ICI"
/clone="8IC8"
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/db_xref="taxon:9606"
/map="19p13.3"
<1. .>97
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19913"
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  STS; myotonic dystrophy
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M14178.1 GI:187097
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Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitsation
Submitsed (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                         26228 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAA 26287
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

( hases I to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Pred. No. 0.021;
0; Mismatches 13; Indels 0
                                                                                                   Score 77.8; DB 11; Length 108;
Pred. No. 0.012;
0; Mismatches 12; Indels 0
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Human sequence tagged site BICBR DNA from 19q13.
X57789
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Human small cytoplasmic Alu transcript.
U67808
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97415756
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/rpt_family="Alu"
/rpt_type=dispersed
37 c 28 g
/rpt_type=dispersed
38 c 26 g
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                                                                                                                                             85; Conservative
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Best Local Similarity
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source

FEATURES

JOURNAL

AUTHORS

TITLE

JOURNAL MEDLINE REFERENCE BASE COUNT ORIGIN

Matches

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DEFINITION

RESULT HS8IC8R

ACCESSION VERSION

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Matches

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ORIGIN

ACCESSION VERSION KEYWORDS SOURCE

LOCUS

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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KEYWORDS

VERSION

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Williamson, R. and Humphriss, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
allurepetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="blood leukocytes from a patient with familial"
1. .108
               Aldridge, F.L.

Direct Submission

Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 47G, UK

Losses 1 to 103)

Butler, R., Riley, J.H., Ogilvie, D.J., Anand, R., Buxton, J.,
Davies, J., Johnson, K. and Markham, A.F.

Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human LDL-receptor mutated gene with intron 12 deletion junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2741 TGCCTGTAATCTCAGCACTCTGGGAGGCCGAGGTAGGTGGATTAGTGGAGGTCATGATTT 2800
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1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alu repetitive sequence; low density lipoprotein receptor
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
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Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 CTTGACCAGCCTGGCCAACATGGTGAAACCCTATCTCTACT 2
                                                                                                                                                                                          Nucleic Acids Res. 19 (17), 4787 (1991) 91367697
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W 83.2%; Pred. No. U.v.-
O; Mismatches
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/clone_lib="YAC library: ICI"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                See also X57788 for STS BIC8L.
                                                                                                                                                                                                                                                                      Location/Qualifiers
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(bases 1 to 103)
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Matches 84; Conservative
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HSLDLRD1/c
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Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens

Eukaryota: Wetazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences

J. Mol. Biol. (1992) In press

Location/Qualifiers
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
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Primates; Catarrhini; Hominidae; Homo.
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/note="LDL-receptor intron D; G00-119-362"
                                                                                                                                                                 DB 9; Length 97; 0.032;
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        42. .72
/gene="LDLR"
/note="deletion target sequence"
/note="deletion target sequence"
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89.0%; Pred. No. 0.03
Live 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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30 c 35 g 1
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/sex="male"
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STS; myotonic dystrophy.
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Gaps

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Length 103;

20-MAY-1992

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Search completed: June 20, 2000, 02:22:00 Job time: 481404 sec
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1 (Dases I to 108)

1 (Dases I to 108)

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See X05250 for corresponding normal gene sequence. In the defective LDL-receptor gene the deletion courred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 14 deletion junction.
                                                                                                        26334 AAAAATTAGCCAGGCATGGTAGCACATGCCTGTAATCCCAGCTACTCAAGAGGCTGAGGC 26393
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Alu repetitive sequence; low density lipoprotein receptor.
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                               Score 74.6; DB 10; Length
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0; Mismatches 19; Indels
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Submission
Submitted (2-405-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OY 15723 GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCGGATCACTTGAAGCCAGGAGTTC 15782
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
                                                                             Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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97415756
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/db_xref="taxon:9606"
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/rpt_type=dispersed
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/note="scAlu"
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June 19, 2000, 11:47:50 ; Search time 580.8 Seconds (without alignments) 12492.804 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-852-495C-2\_COPY\_140000\_169000 29001 1 GGTTTTGACAAAGGTGTCAA......TCCTTCAGGAGTTACTTCTA 29001 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

433070 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 10 Maximum DB seq length: 110

Post-processing: Minimum Match 0% Listing first 45 summaries

N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Human dene signatu	le		Human biallelic po	Human biallelic po	Human biallelic po	Human gene signatu	Human biallelic po	Homo sapiens adult	Human gene signatu	an gene	3' fragment of clo	Human gene signatu	Homo sapiens adult	Human secreted pro	ne sign	Secreted protein C	otide sequ	Human secreted pro	Nucleotide sequenc	Nucleotide sequenc	Human M97-2 secret	Human gene signatu	Probe to internal	Human novel secret	leotide s	3' fragment of clo	Staphylococcus aur	Human secreted pro	Human gene signatu	ED.	secret	adult	Human gene signatu
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	Result No.	c 1	7 0	e	4		0 ن			6	10	c 11	12	13	14	15	c 16	17	18	19	20	21	22	23	24	25	56	27	c 28	58	c 30	31	32	(	c 34

Homo sapiens clone	Human gene signatu	Human gene signatu	Human gene signatu	Human gene signatu	Human biallelic po	Human biallelic po	Human biallelic po	Human gene signatu	Human gene signatu	Human gene signatu
V21226	T24259	T21566	T21566	T26728	X12087	X12085	X12086	T20931	T23131	T23895
-	7	Н	-		_	-	-	-	-	-
69	93	87	87	97	100	100	100	66	95	109
0.5	0.3	0.5	0.3	0.5	0.3	0.3	0.5	0.5	0.3	0.2
55.8	55.8	55.2	55.2	55.2	55.4	55.4	55.4	54.8	54	53.8
		~	<b>&amp;</b>	σ	0	디	2	13	14	5
35	36	m	m	m	4	~	•	•	~	4

## ALIGNMENTS

	07-NOV-1996 (first entry)  Human gene signature HUMGSO7131.  Human gene signature HUMGSO7131.  Gene signature HUMGSO7131.  Call typhig; abnormal cell function; ss.  cell typhig; abnormal cell function; ss.  MO9514772-A1.  101-MOV-1994; J01916.  112-NOV-1994; J01916.  112-NOV-1993; JP-355504.  (MATS.) MATSUBARA K.  (AMDO K.)  MATSUBARA K
	ginature HUMGSO7131. e; messenger RNA; mRNA; relative abundance; frequency; g; mapping; non-biased library; diagnosis; detection; abnormal cell function; ss. JD-35504. BARA K. K. Cokubo K; Cokubo K; 1/27.
	e; messenger RNA; mRNA; relative abundance; frequency; g; mapping; non-biased library; diagnosis; detection; abnormal cell function; ss. JP-355504. BARA K. K. C. Okubo K; 1/27. 1/27. 1/27. 1/27. 0f abnormal cell function, by preparing cDNA that tive abundance of corresp. mRNA in specific human
	g; mapping; non-blased library; diagnosis; detection; abnormal cell function; ss.  J01916.  JP-355504.  BAR K.  Cokubo K;  1/27.  1/27.  1/27.  Of abnormal cell function, by preparing cDNA that tive abundance of corresp. mRNA in specific human
	abnormal cell function; ss.  J01916. BARA K. K. K. Okubo K; A. Okubo K; ene signatures in 3'-directed human cDNA library - e.g of abnormal cell function, by preparing cDNA that tive abundance of corresp. mRNA in specific human
	J01916. JP-355504. K. K. Cokubo K; 1/27. ene signatures in 3'-directed human cDNA library - e.g of abnormal cell function, by preparing cDNA that tive abundance of corresp. mRNA in specific human
	J01916.  JP-355504.  BARA K.  Chubo K;  1/27.  1/27.  Of abnormal cell function, by preparing cDNA that tive abundance of corresp. mRNA in specific human
	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
PA (OKUB/)	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
	3'-directed human cDNA library - e.g function, by preparing cDNA that corresp. mRNA in specific human
	3'-directed human cDNa library - e.g function, by preparing cDNA that corresp. mRNA in specific human
PS Claim	Claim 1; Page 1748; 2245pp; Japanese.
	A single-stranded DNA (or its complementary strand or the corresp.
	e-stranded DNA) which comprises one of the 7837 "GS" sequences
	given in T19001-T26837 and which is able to hybridise to part of
	genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
	nces were obtained from 3'-directed cDNA libraries prepared
	from various human tissues; synthesis of cDNA was initiated from the
CC 3/-end	d of mRNA by using poly(T) as the sole primer. Since the 3'-
	nslated sequence is unique to a particular mRNA species, almost
	he 3'-oriented cDNAs hybridise with specific mRNAs. Each librar
CC is cor	is constructed so as to reflect accurately the relative abundance of
	different mRNAs in the particular tissue from which it was derived.
CC The ap	The appearance frequency of a given GS in a cDNA library can be
	determined (esp. using primers and probes derived from the GS
	sequences) as a means of diagnosing abnormal cell function or for
CC recodu	nising different cell types.
	nce 108 BP; 34 A; 31 C; 26 G; 15 T;
,	
Query Match	Query Match 0.3%; Score 80.4; DB 1; Length 108; Rest Local Similarity 83.3%: Dred No 0.064.
Matches	vative (
. 1000	の300 と思いるとは、そのほうことを見られているとは、これの人がない。 というない というしゅん こうかい かんしゅん こうかん かんしゅう こうかい かんかん かんかん かんかん かんかん かんかん かんかん かんかん か

9951 GCATGACCATGGCTCACTGCAGCCTTGCCCTCCTAGGCTCAAGCAATC 9998 δ g ò qq

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RESULT 2 X12095/c ID X12095 standard; DNA; 108 BP.

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Best Loc
Matches
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 PER 14-7MAY-1996; US-030455.

PR (05-NOV-1995; US-030455.

PR (05-NOV-1996; US-030455.

PR (WHED) DIWHITERED INST BIOMEDICAL RES.

Hudson T, Lander ES, Wang D;

Hudson T, Lander ES, Wang D;

WPI; 98-286974/25.

PR Waising or phenotypic typing for disease

PR (Claim I) Page 219; 310pp; English.

PR (Claim I) Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in CC X10269-X12937 are human DNA fragments which contain biallelic polymorphic CC markers which have been isolated using the primers represented in CC X10269-X12937 are human DNA fragments which contain biallelic polymorphic CC markers which have been isolated using the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for used in methods for determining polymorphic forms in an individual for used in methods for determining polymorphic forms in an individual for used in winch as agammaglobulinemia, diabetes insipidua, Lesch-Nyhan syndrome, cuscopies, paternity testing or for phenotypic typing for diseases used and of standing polymorphic cancer, diseases, hereditary syndrome, osteogenesis inperfecta, acute intermittent porphyria, and syndrome, osteogenesis inperfect, acute intermittent porphyria, anterimment of iseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longwilty, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and suceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic or corpublaxis of such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15725 CTGTAATCCCAGCAC-TTTGGGAGGCCAAGGCAGGCGGATCACTTGAAGCCAGGAGTTCA 15783
             30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CIAIAATCCCAGCACTTTTGGGAGGCCAAGGCAGACGATCACTTGAAGTCAGGAGTTCG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 73.2; DB 1; Length 108;
Pred. No. 0.056;
1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY 15784 AGACCAGCCTGCCCAACATGGCAAAACCCTGGCTCTACCAAAAATACA 15831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24892 standard; cDNA to mRNA; 100 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prophylaxis of such diseases.
Sequence 108 BP; 19 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3
Best Local Similarity 85.2
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsubara K,
                                                                                                             Homo sapiens
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Testing or phenotypic typing for disease

7 determining polymorphic forms for use in e.g. forensics, paternity

7 testing or phenotypic typing for disease

8 Claim 1. Page 219; 310pp; English.

8 X10269-X12937 are human DNA fragments which contain biallelic polymorphic

8 X10269-X12937 are human DNA fragments which contain biallelic polymorphic

8 X10269-X12937 are human DNA fragments which expresented in

8 X10269-X12937 are human DNA fragments which serves the polymorphic site is indicated by

8 X10269-X120268. The base occupying the polymorphic stre is indicated by

8 Control of the proposition of the polymorphic of the servent of the appropriate IUPAC-IUB ambiguity code. These fragments can be used in

8 Control of determining polymorphic forms in an individual for use in

8 Control of the proposition of the proposition of the seases

8 Such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,

8 Control of the proposition of the proposition of the seases, familial

8 Spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary

8 Control of the proposition of the proposition of the nervous

8 Syndrome, osteogenesis imperfecta, acute intermittent porphyria,

8 Syndrome, osteogenesis imperfecta, acute intermittent porphyria,

8 Syndrome, osteogenesis imperfecta, acute intermittent porphyria,

8 Syndrome, infection by pathogenic microcorganisms, and characteristics such

8 System, infection by pathogenic microcorganisms, and characteristics such

8 System, infection by pathogenic microcorganisms, and characteristics such

8 System, infection by pathogenic microcorganisms, and characteristics acute

8 System, infection by pathogenic microcorganisms, and characteristics and characteristics and characteristics and characteristics and characteristics and characteristics and characteristics.
                                                                                                                                                       A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T25837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer, since the 3'-end of mRNA by using poly(T) as the sole primer, since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY 15897 ATCACTTGAACCGGGGAGGCAGAGGTTGCAGTGAGCTGAGATTTCGCCACTACACTACAG 15956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autolimnue disease; cancer; inflammation; drug; therapy; medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ATCGCTTGAACCTGGGAGGCAGAATTTGCAATNAGCTGAGATTGCACCNTTGCACTCCNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid segments from the human genome - used for
for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CCTGGGTGACAGAGTGACACTCTGTTTGAAACAAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.2%; Score 68.8; DB
79.8%; Pred. No. 0.21;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES. Hudson T, Lander ES, Wang D; WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X12095 standard; DNA; 108 BP.
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05-NOV-1997; U20313.
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les 79; Conserv
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WO9820165-A2.
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Matches

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5818 GTGGCTCAAGCCTGTAATCCCAACACTTTGGGAGGCTAAGGTGGGAGGATTGCTTGAGCC 5877
                                                                                                                                                      Human biallelic polymorphic DNA fragment EST98276c.
Polymorphism: biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.

Mo951477-2A.

01-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5878 CAGTAGTTCAAGACCAGCCTGGGCAACATGGAGAAACCC 5916
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Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CAGGAGCTCAAGACCAKCCTGGGAAACATAGCAAGACTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                       14-MAY 1998.
05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
Hudson T, Lander ES, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T24892; standard; cDNA to mRNA; 100 T24892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis of such diseases.
Sequence 100 BP; 22 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%;
                                                                                                                                    30-MAR-1999 (first entry)
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                                                                                                  X12085 standard; DNA; 100
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hes 76; Conservative
                                                                                                                                                                                                                                                         Homo sapiens.
WO9820165-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              While year and the pumper of the pumper of the pumper of the pumper of determining polymorphic forms for use in e.g. forensics, paternity determining polymorphic forms for use in e.g. forensics, paternity are testing or phenotypic typing for disease

Claim 1; Page 219; 310pp; English.

Claim 1; Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the primers represented by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in X09121-X10268. The base occupying the polymorphic stie is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabeters insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Adrich syndrome, Pabry's disease, hereditary spherocytosis, polycystic kidney disease, hereditary papernome, osteogenesis inperfected, acute intermittent porphyria, autolimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                          ij
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                                                                                                                                                                                            18907 TGTATTTTAGTAGAGATAGGGTTTCACAATGCTGGCCAGGCTGGTCTCAAACTCCTGCC 18966
treatments. The isolated polymorphic nucleic acid used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5818 GTGGCTCAAGCCTGTAATCCCAACACTTTGGGAGGCTAAGGTGGGAGGATTGCTTGAGCC 5877
                                                                                                                                                                                                                                                                                                                                                                                                                                           AJO-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGTCTTTTTTGTAGAGATGAGGTTTTCCTRTGTTGGCCAGGATGGTCTCGAACTCCTGAC
                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 100;
                                                                                                                  Length 108
                                                                                                                                                                                                                                                                       Qy 18967 CTCAAGTGATCCTCCTCCTCGGCCTCCC-AATGTGCTGGGATTACAG 19013
                                                                                                                                                                                                                                                                                               61 TICAAGIGATCCGICTGCCTTGCCTCCCAAAGIGCTGGGATTATAG 108
                                                                                                                Score 68.4; DB 1; Length 10
Pred. No. 0.24;
1; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5878 CAGTAGTTCAAGACCAGCCTGGGCAACATGGAGAAACCC 5916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%; Score 63.4; DB 1;
6.8%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                          23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 C;
    drugs or therapeutic treatments.
                                        prophylaxis of such diseases.
Sequence 108 BP; 19 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prophylaxis of such diseases. Sequence 100 BP; 21 A;
                                                                                                                0.2%;
                                                                                                                                                                                                                                                                                                                                                                                           7/c
X12087 standard; DNA; 100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hudson T, Lander ES, Wang D; WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.88;
                                                                                                                                                    89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 76.8
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment; marker; ss
                        can also be
                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                        segments
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Gaps

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22; Indels

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Length 100;

30

22 G;

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09-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease Claim 1; Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity corner These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insiphdus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
                                                                                                                                                  Claim 1: Page 1720; 2245pp; Japanese.

Claim 1: Page 1720; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)

sequences were obtained from 3--directed CDNA libraries prepared
from various human tissues; synthesis of CDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
intranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
Sequence 100 BP; 28 A; 22 C; 25 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18746 TTTTTTTTTTTGAGATGGAGTCTTACTCTGTCGCTCAAGCTGGAGTGCAGTGGCACAATC 18805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human biallelic polymorphic DNA fragment EST98276b.
Polymorphism: biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autolumune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TITGITICAAACAGAGTGTCACTCTGTCACCCAGGCNGGAGTGCAANGGTGCAATC 41
                                                                                   Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1998.
05-NOV-1997; U20313.
06-NOV-1995; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
WHOSON T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18806 TCAGCTCACTGCAACCTCTGCCTTCTGGGTTCAAGCAAT 18844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGCTNATTGCAAATTCTGCCTCCCAGGTTCAAGCGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 62.4; Di
75:8%; Pred. No. 1.5;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X12086 standard; DNA; 100 BP. X12086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 75; Conserv
                                                                     WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                          tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammatory, immuno-stimulatory or suppressing agents
Claim 30; Page 73; 110pp; English.

The sequence is that of an isolated polynuclectide which may
be of use in the production of therapeutic compositions for
treating or ameliorating a medical condition in a mammal. Such
compositions may be used for, e.g. research purposes as markers for
tissues, molecular weight markers for gels, primers or probes, for
nutrition as carbon, nitrogen or carbohydrate source. They can also be
used as a cytokine for cell proliferation and differentiation activity,
as immune stimulants or suppressors, e.g. for viral, bacterial or fungal
infections, for autoimmune diseases such as multiple sclerosis or
systemic lupus erythematosus, to regulate haematopolesis, for tissue
promote, as an activator or inhibitor, or as a chemotactic or
phemotical and apprendiction or inhibitory, or as a chemotactic or
                            syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics suc as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5818 GTGGCTCAAGCCTGTAATCCCAACACTTTGGGAGGCTAAGGTGGGAGGATTGCTTGAGCC 5877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GTGACTCACACCTATAATCCTGGCACTTTAGGAGGCTKAGGAAGGAGGAGTTGTTTGAAAC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding novel secreted proteins - useful as, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens adult retina clone BO365_2 3' region.
adult; retina; cDNA library; clone BO365_2; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62.2; DB 1; Length 100;
Pred. No. 1.5;
0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokinetic, haemostatic and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitor agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%; Score 62.2; DB 1; Length 106; 76.8%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7957 GAAAAGAAACGATCAAGCCATGAAAACACATGAAGGAAA 7995
                                                                                                                                                                                                                                                                                                                 22 G;
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                                                                                                                                                                                                                                                                                                                 25 C;
                                                                                                                                                                                                                                                                             prophylaxis of such diseases.
Sequence 100 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V11611 standard; cDNA; 106 BP
                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1998.
03-0CT-1997. U18007.
04-OCT-1996. US-726237.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.29
Best Local Similarity 76.89
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          suppression; ds
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Query Match
Best Local (
                                                          tissues
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                                                                                                                                                                                                                                                                                                                                                                                               Matches
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A single-stranded DNA (or its complementary strand or the corresp.

A single-stranded DNA, which comprises one of the 787 "GS" sequences
coulde-stranded DNA, which comprises one of the 787 "GS" sequences
coulde-stranded DNA, which comprises one of the 787 "GS" sequences
could war in 119001-126837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
contained of mRNA by using poly(T) as the sole primer. Since the 3'-
conformalisted sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
constructed so as to reflect accurately the relative abundance of
constructed so as to reflect accurately the relative abundance of
configuration of a given GS in a cDNA library can be
configuration of diagnosing abnormal cell function or for
recognising different cell types.

Constructed as means of diagnosing abnormal cell function or for
coconising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15897 ATCACTTGAACCGGGGAGGCAGGGTTGCAGTGAGATTTCGCCACTACACTACAG 15956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATCACTTGAGCCTAGGAGGCAGAGGTTCAAGTGAGCTGAGATGGCACTCCTGCGCTCCAG 61
                                                                                                                                                                                                                                                                                                Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-1996 (first entry)
Human gene signature HUMGS02180.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
WO9514772-A1.
                                                                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%; Score 61; DB 1; Length 91; 78.7%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                            cell typing; abnormal cell function; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 15957 CCTGGGTGACAGAGAGATTCTGTCTCA 15985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T20927 standard; cDNA to mRNA; 103 BP
                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 C;
                                                     F25854 standard; cDNA to mRNA; 91
                                                                                   22-OCT-1996 (first entry)
Human gene signature HUMGS08084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09514 / 2 ...
01-JUN-1994; J01916.
11-NOV-1993; JP-35564.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                         01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70; Conservative
                                                                                                                                                                                                                                                                      Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                   WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jequence recognising differences
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                                                                                                                                                                                                                                                                     Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                       RESULT
T25854
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regulators. Page 70; 114pp; English.

This sequence represents the 3' end of clone M97_2, which is a polynucleotide of the invention. This sequence was isolated from a human neural tissue (glioblastoma line TG98G) cDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or molecular weight marker, in genetic fingerprinting, to raise anti-protein or anti-DNA antibodies and in interaction trap assays. The protein can be used to assay blological activity, raise antibodies for use in immunoassays, as marker, to identify inhibitors of its interactions and as a nutritional supplement. If may also have a very wide range of therapeutic and biological activities (no examples are given to support this), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulant or immunosuppressant, haematopoiesis regulator, bone, cartilage, tendon, ligament and/or nerve tissue growth
                                                                                                                                     Claim 1: Page 758-759; 2245pp; Japanese.
Claim 2: Claim 3: Claim 3: Claim 4: Claim 4: Claim 4: Claim 4: Claim 4: Claim 5: Claim 6: C
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3' fragment of clone M97_2.
Human; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; neural tissue; glioblastoma line TG98G; clone M97_2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGGCAAAACCCTGGCTCTACCAAAAATACAACAATTAGCTGGGCATTGTGGCACATGC 15859
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                e.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins - having many potential uses, e.g. as immunomodulators, cell proliferation or differentiation inhibitors or haematopoiesis regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid clones from ATCC 98028 encode novel secreted
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs K, Lavallie ER, Mccoy JM, Merberg D, Racie LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61.2; DI
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75; Conservative
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19-APR-1996; US-635311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spaulding V;
WPI; 97-535776/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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V61480;
                        RESULT
V11595
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                        haemostatic, thrombolytic or anti-inflammatory agent, antimicrobial, blornythm, metabolism or behaviour modifier, anti-depressant or analgesic or psoriasis treatative.

Sequence 101 BP: 88 A; 0 C; 2 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20049 GATTGCTTAAGCCCAGGAATTTAAGGCTGCAGGGAGCCATGGGGGCCCATTGCACTCCA 20108
                                                                                                                                                                                                                                                                                A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to phybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using polyff as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stimulator, follicle inhibitor/stimulator, chemotactic/chemokinetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.
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Sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marian N. 2010 N. 1879 N. 1879: 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA tha
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Pred. No. 2.5;
0; Mismatches 24; Indels (
                                                                                                                                                                          0.2%; Score 60.6; DB 1; Length 101; 79.1%; Pred. No. 2.5;
                                                                                                                                                                                                                                19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     71 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 101
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Human gene signature HUMGS08452.
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Best Local Similarity 75.8%;
Matches 75; Conservative
                                                                                                                                                                                                  79.18;
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01-UNY-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                     Best_Local Similarity 79.1
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okubo K;
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                                                                                                                                                                             Query Match
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be of use in the production of therapeutic compositions for treating or ameliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers for tissues, molecular weight markers for gels, primers or probes, for nutrition as carbon, nitrogen or carbohydrate source. They can also be used as a cytokine for cell proliferation and differentiation activity, as immune stimulants or suppressors, e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or systemic lupus erythematosus, to regulate haematopolesis, for tissue growth, as an activator or inhibitor, or as a chemotactic or chemokinetic, haemostatic and thrombocytic, receptor/ligand, anti-liflammatory or tumour inhibitor agents.
Sequence 92 BP; 92 A; 0 C; 0 G; 0 U;
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mono sapiens adult testes clone AX65_22 3' end.
adult; testes; cDNA lbrary; clone AX65_22; anti-inflammatory;
therapeutic composition; autoimmune disease; immune; stimulation;
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foetal brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory, immuno-stimulatory or suppressing agents
Disclosure; Page 63; 110pp; English.
The sequence is that of an isolated polynucleotide which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding novel secreted proteins - useful as, anti-inflammatory, immuno-stimulatory or suppressing agents
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This is the 3' polyA sequence of a full-length cDNA clone,
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                                                                                                                                                                                                                                                                                                                                                                                                       Agostino MJ, Jacobs K, Lavallie ER, Mccoy JM, Merberg
Racie LA, Spaulding V, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7958 AAAAGAAACGATCAAGCCATGAAAACACA 7986
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Secreted protein; human; bk95_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.2%;
V11595 standard; cDNA; 92 BP.
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18-MAR-1998; US-040963.
19-MAR-1997; US-820493.
(GEMY ) GENETICS INST INC.
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Best Local Similarity 79.8
Matches 71; Conservative
                                                                                                                                                                                                                                                                                 09-APR-1998.
03-OCT-1997; U18007.
04-OCT-1996; US-726237.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Racie LA, Spaulding
WPI; 98-240082/21.
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                                                                                                                                                                                                                            Homo sapiens
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cc designated bk95_3 (see also V61479), that codes for a novel secreted human protein (see W79089). bk95_3 was isolated from a human adult retina cDNA library using methods which are selective cc for cDNAs encoding secreted proteins, or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the encoding protein. The bk95_3 sequence cc computer analysis of the encoding protein. The bk95_3 sequence shows homology to some database sequences and may include an Alureptitive element. The invention provides cDNA clones (see V61477-87) from human foetal kidney, adult testis, and adult or cc foetal brain cDNA libraries that code for secreted proteins (see W79087-97). These clones are deposited as ATCC 98364. The polynucleotides and proteins are predicted to have useful biological activities which would make them suitable for treating, cc preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional, immune stimulating (e.g. as cc vaccines) or suppressing, haematcopicisis regulating, tissue growth, ctc invasion suppressor and tumour inhibition activities. The cc invasion suppressor and tumour inhibition activities. The cc numour inhibition activities. The conditions are also stated to be useful for gene therapy.
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Query Match
0.2%; Score 60.2; DB 1; Length 92;
Best Local Similarity 79.8%; Pred. No. 2.8;
Matches 71; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 7958 AAAAGAACGATCAAGCCATGAAAACACA 7986

61 AAAAAAAAAAAAAAAAAAAAAA 89

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gb_gss11:*
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1 GGTTTTGACAAAGGTGTCAA......TCCTTCAGGAGTTACTTGTA 29001
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Contact: Wilson RK
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B17434 345K2.TVB C
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AI832832 at72909.x
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                                                                                                                                                                                                                                                                                                                                                                                                  zr25h02.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens SDNA clone IMAGE:664467 3' similar to contains Alu repetitive element; contains element LTR1 repetitive element; n RNA sequence. AA243009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Unpublished (1997)
Description
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E 1 (bases 1 to 106)

S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Walte,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1397630.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.ilnl.gov) for further information.
Insert Length, 1127 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 102.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Matches 98; Conserv
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Gaps

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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 110)
S zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter:@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ386882 110 bp DNA GSS 21-MAY-1999
RPCIII-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
genomic survey sequence.
    /note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1; CalTech Human BAC Library D"
30 c 34 g 17 t
                                                                                                                                                                                                                  QY 11717 GGGTTTCACCATGTTGGCCAGGCTGTTGAACTCCTGACCTCAAGTGATCCACCTGCC 11776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

26 c 38 g 20 t
                                                                                                                                                                                                                                                          1 CCGGCCCCAGACTCTCACGCCTGTAATCCCAGCACTTTGGGAGACCGAGGCGGGTGGATC 60
                                                                                                                                  DB 105; Length 106;
                                                                                                                                                                                                                                                                                                    QY 26270 ACGAGGTCAGGAGATCAAGACCATCCTGGCCAACATGGTGAAACCC 26315
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                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                          61 ACGAGGTCAGGAGATCAAGACCGTCCTGGCTAACATGGTGAAACCC 106
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                                                                                                                              Score 91.6; D)
Pred. No. 0.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/cell_type="Lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens'
/db_xref="GDB:7551267"
/db_xref="taxon:9606"
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AQ386882.1 GI:4357905
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                                                                                                                                                                        97; Conservative
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                                                                                                                                  Query Match
Best Local Similarity
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AQ386882/c
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                                                                                                   Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Luberia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 CACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACGAGGTCAGGAGAT 47
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Other GSSs: CITBI-E1-2509A2.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
711: 301 838 0208
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92.2; DB 37;
Pred. No. 0.17;
0; Mismatches 8;
    primer: -28ml3 revl ET from Amersham
                                                                                      /organism-"Homo sapiens"

    106
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

Seq primer: -28mis iev. ...
High quality sequence stop: 53.
Location/Qualifiers
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/sex="male"
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Best Local Similarity 92.4%;
Matches 97; Conservative
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AA807640.1 GI:2877108
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Best Local Similarity 90.29
Matches 92; Conservative
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AA807640
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E 1 (bases 1 to 105)
S Adams, M.D.; Rounsley, S.D.; Zhao, S., Linher, K., Golden, K., Berry, K., Granger, D., Zuh, E., Wible, C., de. Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Bullding Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search/page:
Seq primer: SP6
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                       AQ282107 105 bp DNA GSS 27-APR-1999
RPCI11-94B21.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-94B21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA807640 103 bp mRNA EST 05-MAR-1998 nx08b05.sl NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255473 3' similar to contains Alu repetitive element; , mRNA sequence.
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/db_xref="GDB:7535756"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="RPCI-11-94B21"
/clone="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCIII Human Male BAC Library"
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                                                                     11; Indels
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Pred. No. 0.6;
0; Mismatches
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Matches 94; Conserv
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: N.L.GAP clone distribution information can be
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
10.1-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP), Tumor Gene Index
Oppublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151346.
Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RPCI-11-317H22.TV RPCI-11 Homo saptens genomic clone
RPCI-11-317H22, genomic survey sequence.
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High quality sequence stop: 87.
Location/Qualifiers
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Pred. No. 0.87;
0; Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

L. Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHil9W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302097, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ003188 110 bp DNA GSS 14-APR-1999
RPCIII-1DIO.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1DIO.
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86.2%; Pred. No. 1.1;
iive 0; Mismatches 15; Indels
                                                                                                                                   /organism-"Homo sapiens"
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/lab_host-"DH10B"
Insert Length: 834 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 63.
Location/Qualifiers
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Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                  Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@deJong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                           2hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20952 CTAGCACTTTGGGAGGCAGAGACAGGCAGATCACCTGAGGTCAGGGGTTTGAGACCAGCC 21011
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae, Homo.
1 (bases 1 to 110)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: Robert-Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 27 c 27 g 18 t
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On Jan 19, 1998 this sequence version replaced gi:2150764.
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.3%; Score 85.4; DB 108; Length 103; 89.3%; Pred. No. 1; Indels 0; Mismatches 11; Indels 0;
                                                                                                                                Unpublished (1997)
Contact: Shaping Jhao, William Nierman, Mark Adams
Contact: Shaping Labo, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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AA897366.1 GI:3033986
        (bases 1 to 103)
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Matches 92; Conservative
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                                                                                                                                                                                                                                                                                                                                              26230 CTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAAGA 26289
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                       /clone="RPC1-1."
/clone=lb="RPC1-11"
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/cell_type="Lymphocytes"
/coll_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
26 g 35 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced g1:1393355.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
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/aev_stage="45 years old"
/lab_host="#65 years old"
/lab_host="DH10B"
/note="vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
bNAse-treated, total callular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tunor Gene Index (1997)
On Nov 29, 1993 this sequence version replaced gi:430513.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA244173 109 bp mRNA EST 20-AUG-1997 coofbu6.s1 NCI_CGAP_Pr1 Homo sapiens CDNA clone IMAGE:1007291 similar to contains Alu repetitive element; mRNA sequence.
                                                                                                                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                     15910 GGGAGGCAGAGGTTGCAGTGAGCTGAGATTTCGCCACTACAG 15956
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                                                                                                                                                                                                                                                                                                                                                                                                             47 GGGAGCCAGAGCTTGCAGTGAGCTGAGATTGAGCCACTGCACTCCAG 1
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High quality sequence stop: 90.
Location/Qualifiers
Average insert size: 1.2 kb."
34 c 26 g 25 t
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                                                                                                                                                                             .2;
                                                                                                                                                                                Pred. No. 1.2;
0; Mismatches
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/clone="InAGE:1007991"
/clone=lib="NCI_CGAP_Pr1"
/sex="Male"
                                                                                                                                                 Score 84.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .LUY
/organism="Homo sapiens"
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                                                                                                                                              Query Match 0.3%;
Best Local Similarity 86.9%;
Matches 93; Conservative
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45 GACCCGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGC 1
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Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dell_line="HeLa cell line; ATCC"
/lab_host="E. coll strain DH5 alpha"
/note="Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT).
From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDC)-mediated cloning strategy."
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Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L.,
Fobbins., C.M., Nussbaum, J.C., Lovett, M. and Green, B.D.
2006 expressed-sequence tags derived from human chromosome
7-enriched cDNA libraries
                                                                                       11671 CCCCTACCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGT 11730
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                                                                                                                                                                                                                                                                                               AA078003 105 bp mRNA EST 24-SEP-1999
*H12D08 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone
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Pred. No. 2.1;
0; Mismatches 14; Indels 0;
                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="7H12D08"
/clone_lib="Chromosome 7 HeLa cDNA Library"
/sex="female"
                                                      Indels
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                                                                                                                                                              DB 30;
               0.3%; Score 84.4; Dilarity 89.2%; Pred. No. 1.3; Conservative 0; Mismatches
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: egreen@nhgri.nih.gov
Plate: 12 row: D column: 08
Seq primer: -2lml3 (ABI).
Location/Qualifiers
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AA078003
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Best Local Similarity
Matches 91; Conserva
                                 Similarity
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                                                  91;
             Query Match
Best Local 9
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Matches
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ESM Homo saplens
EDIATYOTCA; Metrazoa; Chordata; Craniata; Vertebrata; Mammalia;
EDIATYOTCA; Metrazoa; Catarrhin1; Hominidae; Homo.

EURAPOTCA; Metraces; Catarrhin1; Hominidae; Homo.

I (bases 1 to 110)

NoT.-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

No Jan 24, 1997;

On Jan 24, 1995 this sequence version replaced gi:634306.

Contact: Robert Strausberg, Ph.D.

On Jan 24, 1995 this sequence version replaced gi:634306.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@hlh.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Contact Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/lmage.html
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AA244245 110 bp mRNA EST 20-AUG-1997 nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence.
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ilarity 87.4%; Pred. No. 1.9;
Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -41m13 fwd. ET from Amersham
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/clone="IMAGE:1007406"
/clone_lib="NCI_CGAP_Pr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                           AA244245.1 GI:1875104
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Best Local Similarity
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Search completed: June 19, 2000, 21:22:20
Job time: 463507 sec
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                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://Dacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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similar to contains Alu repetitive element; contains element MER31
repetitive element;, mRNA sequence.
                    AQ386882 110 bp DNA GSS 21-MAY-1999
RPC111-13414.TV RPC1-11 Homo sapiens genomic clone RPCI-11-13414,
                                                                                                                                                                                                                                                                   Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                   Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other GSSs: RPCIII-13414.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 82.8; DB 106; Length
Pred. No. 1.9;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/db_xref="GDB:7551267"
/db_xref="taxon:9606"
/clone="RRCI-11-13414"
/clone_lib="RPCI-11"
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                  110 bp
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                                                                            ACCESSION
                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                   AUTHORS
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AQ386882
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                                                                                                                                                                                                                                                                       TITLE
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CDNA Library Arraying: Greg Lennon, Ph.D. Dha Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NII-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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/clone="InAGE:1018256"
/tissue_type="Schwannoma tumor"
/tissue_type="Schwannoma tumor"
/lab_host="Solk (kanamycin resistant)"
/note="Vector: Bluescript SK: Site_1: EcoRI; Site_2:
/note="Vector: Bluescript Site_1: Site_2: Gradator Sequence: Site_2: All Site_2: Site_2:
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

NoT-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Apr 14, 1993 this sequence version replaced gi:639323.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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87.4%; Pred. No. 2.3;
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High quality sequence stop: 96.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
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Best Local Similarity 87.4:
Matches 90; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING STERM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76.8; DB 4;
Pred. No. 1.1e-06;
                             US-08-702-344-22
US-08-44-557C-92
US-08-44-557C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-44-426D-70
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-57
US-08-454-557C-57
US-08-454-557C-57
US-08-454-557C-57
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US-08-450-673C-91
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| Sequence 65, Application US/08481658B
| Patent No. 5995075
| GENERAL INFORMATION:
| APPLICANT: Zavada, Jan
| APPLICANT: Pastorekova, Silvia
| APPLICANT: Pastorekova, Silvia
| APPLICANT: Pastorek, Jaromir
| TITLE OF INVENTION: MN Gene and Protein
| UNMBER OF SEQUENCES: 86
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-0021.3E
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Leona L. Lauder
STREET: 6 Mariposa Court
STATE: 7-10
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TYPE: nucleic acid
STRANDEDNESS: single
       STATE: California
COUNTRY: USA
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US-08-481-658B-65
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10131.958 Million cell updates/sec
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1 GGTTTTGACAAAGGTGTCAA......TCCTTCAGGAGTTACTTCTA 29001
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Listing first 45 summaries

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
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Maximum DB seq length: 110
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Match
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Database :

Result g 

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Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ATTLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
US-08-486-756A-65/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                           26235 ATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAAGACCATC 26294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  Gaps
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                                                                                      105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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83.7%; Pred. No. 1.1e-06;
tive 0; Mismatches 17; Indels
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION A 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORIEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26295 CTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAAA 26338
                                                                                                                                 26295 CTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAAA 26338
                                                                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             US-08-477-504A-65/c
Sequence 65, Application US/08477504A
Patent No. 5972353
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 83.77
Matches 87; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6 Maripose
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
Matches
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RESULT

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Pred. No. 1.1e-06;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                         SOFTWARE: Datentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 26295 CTGGCCAACATGGTGAAACCCCGTCTCTACTAAAATACAAAAA 26338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-0021.3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-485-862B-65/c; Sequence 65, Application US/08485862B; Patent No. 5989838; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
HYPOTHERICAL: NO
ANTI-SPACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                         Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.3%;
Best Local Similarity 83.7%;
Matches 87; Conservative
                                           6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lauder, Leona L. REGISTRATION NUMBER: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L.
                                           STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                   ZIP: 94920
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US-08-486-756A-65
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 83.79
Matches 87; Conservative
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LENGTH: 105 base pairs
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STRANDEDNESS: double
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US-08-481-658B-65
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US-08-787-739-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 ATCCCAGCACTITGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

0.3%; Score 76.8; DB 4; Length 105;
Best Local Similarity 83.7%; Pred. No. 1.1e-06;
Matches 87; Conservative 0; Mismatches 17; Indels (
                                                                                                                                                                OPERATING SISTEM: PC-DOS/MS-LOS
SOFTWARE: PACENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAUGEY, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-435-0737
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRET APPLICATION DATA:
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US-08-787-739-65/C
; Sequence 65, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
APPLICANT: Zavada Jan
; APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
TITLE OF INFORMION: MN Gene and Protein
; UNWBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
                    California
: USA
Tiburon
                                                                 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-485-862B-65
                                            COUNTRY:
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PRIOR APPLICATION DATA:
PRIOR
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAUGET, LEONA L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECHONE: 415-435-2034
TELECHONE: 415-435-2034
                                                       D-0021.3D
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Lauder, Leona L.
REGISTRATION UNUBER: 30,863
REFERENCE/CDCKET NUBBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
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SEQUENCE CHARACTERISTICS:
ENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6 Maripose
CITY: Tiburon
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18903 TTTTTGTATTTTTAGTAGAGATAGGGTTTCACAATGCTGGCCAGGCTGGTCTCAAACTCC 18962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 18963 TGCCCTCAAGTGATCCTCCTGCCTCGGCCTCCCAATGTGCTGGGAT 19008
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/260,190
FILING DATE: 15-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TGACCT--TGTGATCCACCACCACCTCCCCAAAGTGCTGGGAT 105
                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/08477504A
Sequence 65, Application US/08477504A
Sequence 65, Application US/08477504A
Sequence 65, Application US/08477504A
Sequence 7 Savada Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Astorekova, Silvia
APPLICANT: Astorekova, Silvia
COURTES: ADDRESSE: Leona L. Lauder
STATE: California
COUNTRY: USA
                                                                                                                   CORRENT AFFLLCHAILON DAYS:
CORRENT AFFLLCHAILON UNDER:
CLASSIFICATION: 124
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAUGET, LEGNA L.
REGISTRATION NUMBER: 30,863
REFERENCE/CDOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
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US-08-481-658B-65
       MEDIUM TYPE:
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Qy 18903 TTTTTGTATTTTAGTAGAGATAGGGTTTCACAATGCTGGCCAGGCTGGTCTCAAACTCC 18962
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      Length 105;
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                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: US/08/486,756A FILING DATE: US/08/486,756A CLASSIFICATION: 424
Query Match 0.2%; Score 71.2; DB 4; Best Local Similarity 85.8%; Pred. No. 1.4e-05; Matches 91; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                             US-084486-756A-65
US-084486-756A-65
Sequence 65, Application US/08486756A
Selent No. 5991711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INFORMION: NN Gene and Protein
YUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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18903 TTTTGTATTTTTAGTAGAATAGGGTTTCACAATGCTGGCCAGGCTGGTCTCAAACTCC 18962
                                                                                                                                                                                              RESULT 10
US-08-787-739-65
Sequence 65, Application US/0878739
; Patent No. 6027887
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HYPOTHETICAL: NO
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-981-0332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                  18903 TTTTTGTATTTTTAGTAGAGATAGGGTTTCACAATGCTGGCCAGGCTGGTCTCAAACTCC 18962
                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                          ;
                                                                                                                              0.2%; Score 71.2; DB 4; Length 105;
85.8%; Pred. No. 1.4e-05;
tive 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%; Score 71.2; DB 4; Length 105;
85.8%; Pred. No. 1.4e-05;
tive 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94920
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: PREDENTIAL STEM: COMPUTER: PATENTIAL STEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 QY 18963 TGCCCTCAAGTGATCCTCCTGCCTCGGCCTCCCAATGTGCTGGGAT 19008
                                                                                                                                                                                                                                                                                                                            62 TGACCT---TGTGATCCACCAGCCTCGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEGIANT: 2avada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastcrek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Application US/08485862B
Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHANE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO; ANTI-SENSE: NO US-08-486-7568-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                     Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.2
Best Local Similarity 85.8
Matches 91; Conservative
                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
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US-08-485-862B-65
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OCTIVATION DATE:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,566
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
WANDE: TANGOR TROUGHT
                                                                                       QY 18963 TGCCCTCAAGTGATCCTCCTGCCTCGGCCTCCCAATGTGCTGGGAT 19008
                                                                                                                        62 TGACCT--TGTGATCCACCAGCCTCGGCCTCCCAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaronir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Laona L. Lauder
STREET: San Francisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READAELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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GENERAL INFORMATION:
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US-08-450-673C-91/c
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US-08-340-426D-91
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APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITT: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2000-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY 18903 TTTTTGTATTTTTAGTAGAGATAGGGTTTCACAATGCTGGCCAGGCTGGTCTCAAACTCC 18962
                                                               Gaps
                                                                                                                                2 TITITACATCTITAGTAGAGACAGGGTITCACCATATIGGCCAGGCTGCTCTCAAACTCC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                  Length 105;
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                                                                                                                                                                                          Qy 18963 TGCCCTCAAGTGATCCTCCTGGCCTCCCAATGTGCTGGGAT 19008
                                                               13; Indels
                                                                                                                                                                                                                   62 TGACCT--TGTGATCCACCAGCCTCGGCCTCCCAAGTGCTGGGAT 105
               0.2%; Score 71.2; DB 5;
85.8%; Pred. No. 1.4e-05;
tive 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
FILING DATE: 30-MAY-1995
FILING DATE: 30-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 0609.3840003
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-340-426D-91/c
; Sequence 91, Application US/08340426D
; Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                               Sequence 91, Application US/08454557C
Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 26285 CAAGACCATCCTGGCCAACATGG 26307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 86.7
Matches 72; Conservative
                                                               Conservative
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                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        US-08-454-557C-91/C
                                                          91;
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                                                            Matches
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Patent No. 594888
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Alzheimer's Disease
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STRATE: D.C.
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 0609.3840002
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: NOCHOLE CACHA
TYPE: NOCHOLE CACHA
TYPE: DOCK
TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65.4; DB 4;
Pred. No. 0.00017;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.2%;
Best Local Similarity 86.7%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-3934
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APPLICANT: ECKET, David J.
APPLICANT: ECKET, David J.
APPLICANT: Extern David J.
APPLICANT: Extern David J.
APPLICANT: Berg, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Miegaard, Niels E.
APPLICANT: Miegaard, Niels E.
APPLICANT: Miegaard, Niels E.
APPLICANT: Miegaard, Niels E.
APPLICANT: Miegard, Niels E.
APPLICANT: Miegard, Niels E.
APPLICANT: Miegard, Niels E.
APPLICANT: Miegard, Niels E.
APPLICANT: NIELS MIEGARD OF PEPTIDE
TITLE OF INVENTION: WIELE ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 98;
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 19930702
CLASSIFICATION: 435
PRIOR APPLICATION WHERE: Q8/054,363
FILING DATE: 26-APRIL-1993
ATTONEX/AGENT INFORMATION:
ANAMERICATION COMPATION:
ANAMERICATION COMPATION COMPATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

0.2%; Score 62.8; DB 1;
Best Local Similarity 77.6%; Pred. No. 0.00059;
Matches 76; Conservative 0; Mismatches 22;
                                                                                                                                 Score 65.4; DB 6;
Pred. No. 0.00017;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISIS-1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-088-658-42; Sequence 42, Application US/08088658; Sequence 42, Application US/08088658; Patent No. 5641625; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CGACACCAGCCTGATGAACATGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DCCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELERAX: 215-568-3439
                                                                                                                                 0.2%;
                                                                                                                                 Query Match 0.2
Best Local Similarity 86.7
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One Libert CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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ZIP: 19103
                              PCT-US95-17111A-91
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PCT-0595-17111A-91/C

Sequence 91, Application PC/TUS9517111A

Sequence 91, Application PC/TUS9517111A

Sequence 91, Application PC/TUS9517111A

SEQUENCE 91, Application PC/TUS9517111A

SETILE OF INVENTION: Burnal Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

CONTRY: JUSAA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65.4; DB 4;
Pred. No. 0.00017;
0; Mismatches 11;
                                            FILING DATE: 30-WAY-1995
CLASSIFICATION: 530
ATTONREY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFRENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDENESS: both
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REGISTRATION NUMBER: 36, 203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                           APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CGACACCAGCCTGATGAACATGG 1
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86.7%;
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Best Local Similarity 86.7%
Matches 72; Conservative
CURRENT APPLICATION DATA:
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Search completed: June 20, 2000, 02:28:19 Job time: 480829 sec

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1 ATTTACAGATGGAGAAAACCA.......GGATTĀGGGATCATGATCTC 29001
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Human		XO5251 Human LDL-r	Human c	X05249 Human LDL-1	X05251 Human LDL-r	Human c	Human	U67808 Human smal	M87924 Human carci	O		Human	U67807 Human small	Human c	Human	L30244 Human STS	Human l	Human		WIAF-2	t Human	M8/900 Human carci	Hor	Huma	U67806 Human smal	Human ]		3			ø	Human	Human H	ALL-1	L30306 Human STS U	AF185109 Lasiorhin	9	Human fami	I	H.sapi	
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1 (bases 1 to 108)

1 (bases 1 to 108)

1 Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.

Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. 3. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
Bur. J. Blochem. 164 (1), 77-81 (1987)
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                                            20-MAY-1992
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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                                                               Human LDL-receptor gene intron 14 fragment (normal gene).
                                                                                                                         Alu repetitive sequence; low density lipoprotein receptor
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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RESULT 1
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*Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNa.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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//Organism="Homo sapiens"
//db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Blochem. 164 (1), 77-81 (1987)
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deletion junction.
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1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
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Alu repetitive sequence; low density lipoprotein receptor.
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87.9%; Pred. No. 40-05.
                                                                                                                                                                              Qy 19132 GCAGGAGAATCACTTGAACCCAGGAGGCAGAGATTGCAGTGAGCTGAG 19179
  Length 108;
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                                                                                                                                                                                                     61 GCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAG 108
                                           10; Indels
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Human LDL-receptor mutated gene with intron 14
X05251
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0; Mismatches 13;
Score 92; DB 10;
Pred. No. 4.2e-06;
                                             0; Mismatches
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  0.3%;
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Best Local Similarity 87.20,
Conservative
Conservative
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                                             Conservative
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  Query Match
Best Local Similarity
Matches 98; Conserv
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HSLDLRD1/c
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See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                 Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)

    1. .108
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /cell_type="blood leukocytes from a patient with familial"
    1. .108

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1 (basea 1 to 107)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcriptional selection of master sequences
J. Mol. Biol. (1992) In press

Location/Qualifiers
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                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Human carcinoma cell-derived Alu RNA transcript,
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4e-05;
13;
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Pred. No. 0.00012;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NRera2D1"
/dev_stage="embryo"
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30 c 35 g 1
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89.18;
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Best Local Similarity
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Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
L. Bur. J. Blochem. 164 (1), 77-81 (1987)

E 87161901

*source: hypercholesterol aemia
See X65248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
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QY 19131 GGCAGGAGAATCACTTGAACCCAGGAGGCAGAGATTGCAGTGAGCTGAGATCGCGCCCACT 19190
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 108)
                            Alu repetitive sequence; low density lipoprotein receptor.
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Pred. No. 0.00014;
0; Mismatches 15; Indels
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19157 GGCAGAGATTGCAGTGAGCTGAGATCGCGCCACTGCATTCCAG 19199
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/.cell_type="blood leukocytes from a patient with familial"
1..108
//note...

                           Williamson, R. and Humphries, S. Minequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
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1 (Abasa 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcriptis in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy 19072 ACAAAATTAGCCAGGCCTGGTGGCATCTGCCTGTAGTCCCAGCTACTCGGGACACTGAG 19131
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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   Dunning, A., Havinga, J.R.,
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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Pred. No. 0.00014;
0; Mismatches 15; Indels
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Pred. No. 0.00019;
                                                                                                                                     Eur. J. Biochem. 164 (1), 77-81 (1987) 87161901
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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Horsthemke, B., Beisiegel, U.,
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
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1 (bases I to 108)
Shakkh, T. H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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61 GCCGGAGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAG 103
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Human small cytoplasmic Alu transcript.
U67808
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Human small cytoplasmic Alu transcript.
U67803
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97415756
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/db_xref="taxon:9606"
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/rpt_type=dispersed
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1. 108
/note="scAlu"
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Location/Qualifiers
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1 (base) 1 to 107)
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Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                        QY 18966 GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTTTGA 19025
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                                                                                                                                                                                                                                                                                                                                                                            1 GCCTGTAATCCCAGCACTTTGGGAGGCCAAGTCGGGTGGATCACAAGGTCAGGAGTTTGA 60
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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Homo sapiens
                                                                                                                                                                                                                                                                                        Score 81; DB 11; Length 108;
Pred. No. 0.0003;
0; Mismatches 10; Indels
 Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.3%; Score 78; DB 9; Length 107
Best Local Similarity 85.3%; Pred. No. 0.00094;
Matches 87; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OY 19026 GACCAGCCTGACCAACATGGTGAAACCCTGTCTTAC 19062
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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                                                                                             1. .108
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu7"
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30 c 35 g 1
                                                                                                                                                                                       /rpt_family="Alu"
/rpt_type=dispersed
                                                                                                                                                                             /note="scAlu"
                                                                                                                                                                                                                                                                                          0.3%;
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Matches 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSLDLI12 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
                                                                                                                                          Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Pred. No. 0.0011;
0; Mismatches 14; Indels
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualiflers
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38 c 20 g 29 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 q 1
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/sex="male"
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86.0%;
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Best Local Similarity 86.0
Matches 86; Conservative
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Search completed: June 20, 2000, 17:56:59 Job time: 537503 sec
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Frimates; Catarihini; Hominidae; Homo.

(CE 1 (bases 1 to 103)

(NE 1 (bases 1 to 103)

(NE 2 (bases 1 to 103)

(NE 3 (bases 1 to 103)

(NE 4 (bases 1 to 103)

(NE 5 (bases 1 to 103)

(NE 6 (bases 1 to 103)

(NE 7 (bases 1 to 103)

(NE 8 (bases 1 to 103)

(NE 8 (bases 1 to 103)

(NE 9 (bases 1 to 103)

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                                                                             17548 TTGGTTCACTGCAACCTCTGCCTCCTGGGTTCAAGCGATTCTTCTGCCTCAGTCTCCTGA 17607
                                        Gaps
                                                                                               2 TCGCCTCACCACAACCTCTGCCTCTGGGTTCAAACCATTTTCCTGCCTCAGCCTCTA 61
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DB 10; Length 108;
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Query Match 0.3%; Score 76.6; DB 10; Length : Best Local Similarity 82.2%; Pred. No. 0.0016; Matches 88; Conservative 0; Mismatches 19; Indels
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Human sequence tagged site BICBR DNA from 19q13.
X57789
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Best Local Similarity 84.2%; Pred. No. 0.0021;
Matches 85; Conservative 0; Mismatches 16.
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Human small cytoplasmic Alu transcript.
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/clone_lib="YAC library: ICI"
/clone="8IC8"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            x57789.1 GI:23938
STS: myotonic dystrophy.
human.
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U67807.1 GI:2289921
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HSU67807/c
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Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Burect Submission
Submitted (12-406-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY 17338 GTAGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGGGAT 17397
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
Shaikh, T. H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scalu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 11; Length 110;
Pred. No. 0.003;
0; Mismatches 15; Indels
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97415756
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                                                                                                                                                                                                                                                                                                                             1. 110
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
/rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="scAlu"
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84.8%;
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Best Local Similarity 84.8%
Matches 84; Conservative
                                                                                                                 transcripts
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WHISD 98-286694/4725.

WHISD OF JANDER COURS for use in e.g. forensics, paternity determining polymorphic forms for use in e.g. forensics, paternity resting or phenotypic typing for disease

Claim 1; Page 219; 310pp; English.

CX 10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in CX 1021-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in CX 09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases cuch as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, hereditary spherocytosis, von Willebrand's disease, therefultary and sucception of cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such cautoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such cautoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics candurance, fertility, and susceptibility or receptivity to particular culture context can also be used to produce medicaments for the treatment or receptivity is and susceptibility or ecceptivity to particular context of endrances.
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                                                                                                                                          Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autofimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

WO9514772-A1.
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Pred. No. 0.034;
1; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T25009 standard; cDNA to mRNA; 108
                X12095/C

ID X12095 standard; DNA; 108 BP. AZ X12095/C

T 30-MAR-1999 (first entry)

E Human biallelic polymorphic DNA

Polymorphism; biallelic; human;

W detection; phenotypic typing; of

A autoimmune disease; cancer; inf

W treatment; marker; ss.

NW 09820165-A2.

PR (WHED) WHITEHEAD INST BIOMEDIC)

PR (G-NOV-1996; US-030455.

PR (G-NOV-1996; US-030455.

PR (WHED) WHITEHEAD INST BIOMEDIC)

PR (WHED) WHOTHEREAD INST BIOMEDIC)

PR (WHED) WHITEHEAD INST BIOMEDIC WHITEHEAD INST BIOMEDIC WENGENED CONTONING C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ОКИВ/) ОКИВО К.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T25009
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Detection of polymorphic genetic markers of the form

Detection of polymorphic genetic markers of the form

(dc-dA)n(dG-dTyn - using novel nucleic acid mols. as primers

Sample 8; Column 57-58; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences

thaving the sequence (dc-dA)n.(dG-dTyn which can be used as genetic

markers. Primers based on these sequences can be used to detect these

repeats, especially for use in e.g paternity or maternity testing,

thuman genetic analysis such as linkage analysis of genetic disease,

commercial animal or plant breeding or pedigree analysis.

The repeats, when analysed, fall into 4 categories:

The repeats which are alternating tandem CA repeats with no

interruptions and without adjacent repeats of another sequence;

interruptions and without adjacent repeats of another sequence;

imperfect repeats which are defined as 2 or more runs of uninterrupted

CA repeats separated by no more than 3 consecutive non-repeat bases;

S compound perfect repeats which are uninterrupted runs of CA separated
                                                                                                                                                                                Claim 1, Page 1748; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA, which comprises one of the 7837 [63s sequences of given in T19001-T25687] and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end than a sole primer is neglected, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular rissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 34 A; 26 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21268 TTTTTTTTTTTTTTTTTTTAGGCAGAGTCCTACTCTGTCACCCAGGCTGGAGTGCAGGG 21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (dC-dA)n.(dG-dT)n polymorphic repeat sequence #12.
Polymorphism: repeat sequence, genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 TTTGNTGTTGTTGTTGTTTTCAACAGGGTCTTGCTCTGTCACTCAGGCTGGAATNCAGTG 49
                        WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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0.2%; Score 67.6; DB 1; Length 108;
Best Local Similarity 75.9%; Pred. No. 0.074;
Matches 82; Conservative 0; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY 21328 GTGTGAACATGGCTCACTGCAGCCTCAACCTACTGAGCTCAAGCAATC 21375
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21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
Okubo K;
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US5582979-A.
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by no more than 3 consecutive non-repeat bases from a run of at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dC-dA)n.(dG-dT)n, or from at least 10 uninterrupted monoucleotides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect scompound repeats except that the runs of CA are interrupted. This sequence is an example of a compound imperfect repeat sequence of structure: T(CT)12GTT(TC)11T(CA)14A(AC)6. Sequence 92 BP: 21 A; 43 C; 1 G; 27 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY 19140 ATCACTTGAACCCAGGAGGCAGAGATTGCAGTGAGCTGAGATCGCGCCACTGCATTCCAG 19199
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ATCGCTTGAACCTGGGAGGCAGAATTTGCAATNAGCTGAGATTGCACCNTTGCACTCCNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA, mRNA, relative abundance, frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as means of diagnosing abnormal cell function or for recognishing different cell types.

Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Claim 1; Page 1720; 2245pp; Japanese.
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Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                       0.2%;
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Best Local Similarity 93.19
Matches 67; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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T24892
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QY 19200 CCTGGGAGACAGAGCGAGACTCCATCTCAAAATTAAAAA 19238

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Laine 1: Page 1720; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "63" sequences

given in T19001-T26837 and which is able to hybridise to part of

human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

curranslated sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for
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                                                                                                                                                                                                                                                                                                                                                                                                                              - e.g.
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13-Wov-1996 (first entry)
Human gene signature HUMGS08452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
Gene signature; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                 Gene signature: messenger RNA; mRNA; relative abundance; frequency; human; cloning: mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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62 CCTGGGTGACAGAGTGACACTCTGTTTGAAACAAA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62.4; DB
Pred. No. 0.41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; cloning; mapping; non-biased libra
cell typhing; abnormal cell function; ss.
Homo sapiens.
WQ9514772_Al.
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                                                                                                                 T24892 standard; cDNA to mRNA; 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recognising different cell types. Sequence 100 BP; 28 A; 22
                                                                                                                                                     05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                    Okubo K;
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Best Local Similarity
                                                                                                                                                                                                                                                                  W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                        Matsubara K
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                                                                                                                                   T24892;
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T26213
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RESULT
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                                                                                                                                                                             A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in Tigodi-T26837 and which is able to hybridise to part of part of the min Tigodi-T26837 and which is able to hybridise to part of them min Tigodi-T26837 and which is able to hybridise to part of them of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3512 ATGACTTGAGCTCCGGAGGGGGGGGGTTGCAGTGAGCCCAGATTACACCACTGCACTCCAG 3571
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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the 7837 "GS" sequences given in T19001-T25837 and which comprises one of the 7837 "GS" sequences given in T19001-T25837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA ilbraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                        e.g.
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Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss.

WO9514772-A1.
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Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.6; DB 1; Length 103;
Pred. No. 0.38;
0; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2029; 2245pp; Japanese.
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T21566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.2%;
Best Local Similarity 76.2%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1995.
12-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
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                                         WPI; 95-206931/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A single-stranded DNA (or 1fs complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from warious human tissues; synthesis of cDNA hibraries prepared from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
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                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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Sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. Sequence 87 BP; 35 A; 21 C; 16 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                        0.2%; Score 61.6; DB 1; Length 87;
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                                                                                                                                                                                                                                                                      Pred. No. 0.53;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T20927 standard; cDNA to mRNA; 103 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy 17373 TCTCGAACTCCTGGCCTCAAGCGATC 17398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 TTTTAAACTCCTGGGNTCAAGCGATC 1
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Human gene signature HUMGS02180.
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Matches 70; Conservative
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Best Local Similarity 75.8°
Matches 75; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okubo K;
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                                                                                                                                                                                                                                           Query Match
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Homo sapiens.
WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                     A single-stranded DNA (or its complementary strand or the corresp.
A single-stranded DNA) which is able to hybridise to part of
double-stranded DNA) which is able to hybridise to part of
stranded DNA) which is able to hybridise to part of
double-stranded DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
c given in T19001-T28837 and which is able to hybridise to part of
thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
c sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
c 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
c all the 3'-oriented cDNA hybridise with specific mRNAs. Each library
c is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
CT he appearance frequency of a given GS in a cDNA library can be
cc determined (esp. using primers and probes derived from the GS
c sequences) as a means of diagnosing abnormal cell function or for
ce recognishing different cell types.
Squence 108 BP; 18 A; 33 C; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18934 AAICAAIAACIAGGCIGGGCGIGAIGGCICACGCCIGIAAICCCAGCACTIIGGGAGGCC 18993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                              14-NOV-1996 (first entry)

Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene signature HUMCSO8452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cull typing; abnormal cell function; ss.
HOMO saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 61.4; DB 1; Length 108; 79.8%; Pred. No. 0.57;
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ID T26213 standard; cDNA to mRNA; 103 BP
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                         18/c
126828 standard; cDNA to mRNA; 108
126828;
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                                                                                                                                                                        11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K. Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 79.8
Matches 71; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
MATSUBARA K, Okubo K;
WPI; 95-206931/27.
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                                                                                                                                                  W09514772-A1.
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A single-stranded DNA, which composementary strand or the corresp.

C double-stranded DNA, which composes one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
c is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
c sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
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Human gene signature HUMGS04188.

Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 C;
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                                                                                                                                                                            Claim 1; Page 2029; 2245pp; Japanese.
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Best Local Similarity 75.2
Matches 76; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
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14-NOV-1996 (first entry)
Human gene signature HUMGS09078.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
HOMO Sagiens.
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21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                                                  11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                        Okubo K;
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US5582979-A.
                                                                                                                                                 W09514772-A1.
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                                                                                                                                                                    01-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA libraries prepared from various human tissues; synthesis of cDNA as initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular is constructed and the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Human gene signature HUMG/S08084.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss.

WO9514772.Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                          Length 93;
                                                                                                             21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 T;
                   22 T;
                                                                          Score 60.6; DB 1;
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                                                                                                                                                                                                                        21343 ACTGCAGCCTCAACCTACTGAGCTCAAGCAATC 21375
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                                                                                           Pred. No. 0.74;
                                                                                                             0; Mismatches
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                   24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1944; 2245pp; Japanese.
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                   23 C;
                                                                                                                                                                                                                                                                                                                                                    T25854 standard; cDNA to mRNA; 91
cell types
                                                                        0.28;
                   22 A;
                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1996 (first entry)
                                                                                                             72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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 different
                                                                        Query Match
Best Local Similarity
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nes 69; Conserv
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recognising
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                     Sequence
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T25854
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RESULT T26828

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA hibraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-entranslated sequence is unique to a particular mRNAs ince the 3'-entranslated sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 18 A; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2708 GATCTCTCGACCTTGTGATCCACCGGCTCAGCCTCCCAAAGTGCCAGGATTACAGGCAT 2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd67.
Polymorphism; repeat sequence, genetic marker; primer; amplification;
PGR; polymerase chain reaction; paternity; maternity; human; pedigree;
Linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.2%; Score 59.4; DB 1; Length 108; 72.8%; Pred. No. 1.1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2768 GAGCCACCGTGCCCAGCCTCTTTTCTTTTCTTATAAGACAAG 2810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GAGCCACCACGCCCGGCTGTTTTTTTTTTATAACTGTACAGG 103
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0; Mismatches
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PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

Disclosure; Column 11-12; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences

CC markers. Primers based on these sequences can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC repeats, especially for use in e.g paternity or maternity testing,

CC human genetic analysis such as linkage analysis of genetic disease,

CC commercial animal or plant breeding or pedigree analysis. Clones

CC containing the repeat sequences were isolated by hybridisation of

CC chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT)

CC chromosome-specific phage libraries with a synthetic poly(dC-dA). (dC-dT)

CC chromosome-specific phage libraries with a synthetic poly (dC-dA). (dC-dT)

CC chromosome-specific phage libraries with a synthetic poly (dC-dA). (dC-dT)

CC sequence hap primers T65798-T66047. Those clones where the repeat

CC sequence having the formula: (TC)12(AC)18.

CC sequence having the formula: (TC)12(AC)18.

SQ Sequence (60 BP; 18 A; 30 C; 0 G; 12 T;
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Search completed: June 20, 2000, 18:25:24 Job time: 538035 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                             June 19, 2000, 21:22:20 ; Search time 13789.4 Seconds (without alignments) 8524.491 Million cell updates/sec
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29001
1 ATTTACAGATGGAGAAACCA.......GGATTAGGGATCATGATCTC 29001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Unpublished (1997)
Other_GSSs: CIT-HSP-2017G2.TFB
Conteat: Mark Adams
Conteat: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: medical Series (info@resgen.com). BAC end search page:
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.ligr.com/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                    Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contact Pieter de Jong
(pieter@dejong mae.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Essarch Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                       18960 GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGACACATCACGAGGTCAGGA 19019
                                                                                                                                                                                                                        /cloue________/sex="Male"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
*An q 18 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B65160 108 bp DNA GSS 21-JUN-1998
CIT-HSP-2017G2.TRB CIT-HSP Homo saplens genomic clone 2017G2,
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 105; Length 105;
                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GTACGAGACCAGCCTGACCAACATGGTGAAACCCCGTCTACTA 105
                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                    Score 89; DB 10
Pred. No. 0.34;
0; Mismatches
                                                                                                                                     Location/Qualifiers
1. 105
/organism="Homo sapiens"
/db_xref="GDB:7535756"
/db_xref="taxon:9606"
/clone="RPCI-11-94B21"
/clone_lib="RPCI-11"
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1. .108
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Best Local Similarity 90.5%;
Matches 95; Conservative
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B65160,1 GI:2639138
                                                                                                               Seq primer: SP6
Class: BAC ends
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AUTHORS
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COMMENT
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KEYWORDS
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B15423 345B10.TV C
AA835205 ak64h01.s
AA812141 ob48h02.s
AQ414071 RPCI-11-1
                                               AQ028426 CIT-HSP-2
AA703692 ag81a10.r
AA583697 nD58f10.s
AI991750 wt48e01.x
AA385808 EST99495
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N25299 yw52c09.sl
AA244245 nc07a04.s
AA244245 nc07a04.s
AA565533 nk42b11.s
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AA218889 zq15d04.s
B17434 345K2.rvB c
AQ028426 CIT-HSP-2
B65160 CIT-HSP-201
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AA654562 nt75f10.s
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H67040 yu68c01.rl
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AQ282340 RPCI11-80
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AQ634950 RPCI-11-4
AA252633 zq43g05.r
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AQ544583 CITBI-E1-
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AQ200347 RPCI11-43
                                                                                                                                                                                                                                                                                                                                                                                       AQ584425 RPCI-11-4
AQ321855 RPCI11-11
                      AQ282107 RPCI11-94
365160 CIT-HSP-201
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AA243009 zr25h02.s
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AI249096 qh73g09.x
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AA897366 am06h02.s
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H67040 vn68c01 +1
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPCI11-4N6.
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RPCI11-94B21.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-94B21,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AA252633
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AQ282340
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AQ321855
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H67040
AA243009
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B65160
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AQ282107
AQ282107.1 GI:3907976
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 109)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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Sucon, M. and Venter, J.C.

Building (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                    108 AGTGTGCAGTGGTATGATCTTGGCTCACTGCAACCTCCACCTCCCGGGTTCAAGAGATTC 49
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/clone_11b="CTT-HSP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
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Pred. No. 0.36;
0; Mismatches 12; Indels
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Score 87.2; DB 94; Length 109; Pred. No. 0.54;

0.3%;

Query Match Best Local Similarity

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XhoI; Cloned unidIrectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 kb; Uni-ZaP XR vector; -5' adaptor sequence: 5'
GTCGAGTTTTTTTTTTTTTTTTTTT" 3'"
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                                                                                                                                                                                                                                                                                                                      AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
24586 TTTTTCTGAAATGGAGTCTCACTCTGTTGCCCAGGCTGGAGTACAGTGGCACAATCTTG 24645
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Karzman, D., Kucaba, T., Lacy, M., Lehnon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Unpublished (1977)
On Sep 12, 1996 this sequence version replaced gi:1397630.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
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                              2 TGTTTTCTGAGACGGACTCTCACTCTGTCACCCCAGGCTGGAGTGCAGTGGCACAGTCTGA 61
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4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                QY 19023 TGAGACCAGCCTGACCAACATGGTGAAACCCTGTCTTACTAACAA 19068
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
LNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #:
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1133359.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2510712"
/clone_lib="NCI_CGAP_Pan1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"/db_xref="taxon:9606"
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High quality sequence stop: 62.
Location/Qualifiers
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AA385808
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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A1991750
A1991750.1 G1:5838578
EST.
                                      AA583697 101 bp mRNA EST 26-SEP-1997 nn58f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1088107 3' similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                      18962 TCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGT 19021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692704.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergfhih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB 35; Length 101;
Pred. No. 0.98;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 TCGAGATCAGCCTGGCCAACATGGTGAAATCCCGTTTCTAC 1
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High quality sequence stop: 93.
Location/Qualifiers
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/clone="IMAGE:1088107"
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                                                                                                                  AA583697.1 GI:2368306
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1 Similarity 90.1%;
91; Conservative (
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Best Local Similarity
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A1991750/C
LOCUS
DEFINITION
RESULT 5
AA583697/c
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AUTHORS
TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 107)

2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.H., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA385808 107 bp mRNA EST 21-APR-1997
EST99495 Thyroid Homo sapiens CDNA 5' end similar to EST containing
                                                                           ö
                                                                                                                                              3343 AATCCTAGCACTTTGGGAAGCCGAGGGGGGCAGATCACCTGAGGTCAGGACTTTGAGACC 3402
                                                                              Gaps
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   Length 106;
                                                                       13; Indels
                                                                                                                                                                                                                                                                                         3403 AGCCTGACCAACATGGCAAAACCTCATCTTACTAAAAATACAAAA 3448
                                                                                                                                                                                                                                                                                                                               DB 63;
Score 85.2; DB Pred. No. 0.91; 0; Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 109)

Hillier,L. Lennon,G. Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N25299 109 bp mRNA EST 28-DEC-1995
yw52c09.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone
IMAGE:255856 3' slmilar to contains Alu repetitive element;, mRNA
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97044478
                                                                                                     Email: est@watson.wustl.edu
Insert Size: 1316
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
Insert Length: 1316 Std Error: 0.00
Seq primer: MI3RPl
High quality sequence stop: 363.
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             444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85; DB 22; Length 109;
Pred. No. 0.95;
0; Mismatches 15; Indels
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/clone_lib-"Soares infant brain lNIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:419851"
/db_xref="taxon:9606"
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Best Local Similarity 86.2%;
Matches 94; Conservative (
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                                         Tel: 314 286 1800
Fax: 314 286 1810
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Bednarik, D. P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

for clone availability additional sequence available availability additional availability availability availability availability additional availability availability additional availability availability availability additional availability availability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: thyroid gland; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI" 34 c 28 g 26 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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1 (bases 1 to 109; Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                           On Jan 25, 1995 this sequence version replaced gi:637865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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On May 5, 1995 this sequence version replaced gi:798506.
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.3%; Score 84.8; DB 33; Length 107;
86.0%; Pred. No. 1;
tive 0; Mismatches 15; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .107
/organism="Homo sapiens"
/db_xref="Arcc (inhost):189984"
/db_xref="taxon:9606"
/clone_lib="Thyroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H11143
H11143.1 GI:875963
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nes 92; Conservative
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COMMENT
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Gaps

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Seq primer: -41m13 fwd. ET from Amersham
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Unpublished (1997)
On Jan 24, 1995 this sequence version replaced gi:634306.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Genome distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19130 AGCCAGGAGAATCACTTGAACCCCAGGAGGCAGAGATTGCAGTGAGCTGAGATCGCGCCAC 19189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria: Primates; Catarrhini; Hominidae, Homo.
1 (bases 1 to 110)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                             Email: est@watson.wustl.edu
Source: TMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 307.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AGGCAGGAGAATGCCAGGAACCTGGGAGGCAGAGTTTGCAGTGAGCAGAGATCACGCCAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA244245 110 bp mRNA EST 20-AUG-1997 nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence.
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                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 85.2; DB 24; Length 109;
Pred. No. 0.9;
0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                    /organism-"Homo sapiens"
/db_xref="CDB:3866265"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                         /sex="Female"
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AA244245.1 GI:1875104
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.3
Matches 93; Conservative
                                                       Tel: 314 286 1800
Fax: 314 286 1810
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/dew_stage="45 years old"
/dew_stage="45 years old"
/lab_host="pullOB"
/note="vector: pAMPIO; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMPIO by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman.
17 a 26 c 28 g 38 t 1 others
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Unpublished (1997)
On Jan 24, 1995 this sequence version replaced gi:634306.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                      Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 90.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 0.95;
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                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1007406"
/clone_11b="NCI_CGAP_Prl"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%;
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AA244245.1 GI:1875104
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Matches 94; Conserv
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Gaps

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18-MAY-1999

source

FEATURES

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Venue.J.U.:
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Email: bbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.mec.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                            19093 TGGCATCTGCCTGTAGTCCCAGCTACTCGGGACACTGAGGCAGGAGAATCACTTGAACCC 19152
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                       Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ535244 103 bp DNA GSS 18-
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
AQ535244 1GI:4846934
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                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 84.6; DE ilarity 86.9%; Pred. No. 1.1; Conservative 0; Mismatches
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/organism="Homo sapiens"
                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Matches 93; Conserv
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                                                                                                                                                                                          /dev_stage="45 years old"
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/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
bNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptor: 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UGS-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
17 a 26 c 28 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Arraying: Greg Lennon, Ph.D. Days Sequencing Center by Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CEAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393355.
Contact: Robert Strausberg, Ph.D.
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nk42bll.sl NCI_CGAP_GC2 Homo sapiens CDNA clone IMAGE:1016157 3' similar to contains Alu repetitive element;, mkNA sequence.
AA565533.1 GI:2337172
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
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High quality sequence stop: 87.
Location/Qualifiers
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/clone="InAGE:1007406"
/clone_lib="NCI_CGAP_PrI"
/sex="Male"
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ity sequence stop: 90.
Location/Qualifiers
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Matches 94; Conservative
     High quality
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RESULT 12 AA565533/c DEFINITION ORGANISM

ACCESSION

VERSION KEYWORDS SOURCE

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

Query Match

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BASE COUNT

ORIGIN

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62 GTGTGGTGGCGCACGCCTGTGATCCCAGCTACTCGGGAGGCTGACGCA 109
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E I (bases 1 to 109)

S Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Urpublished (1998)

C ontart. Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library BCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Resoarch Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                AQ200347 109 bp DNA GSS 20-APR-1999
RPCI11-43B21.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-43B21,
genomic survey sequence.
AQ200347
                                                                                                                                                    19961 CCAGCACTTTTGGAGGCCGAGGCGTGCAGATCACTTGAGGACAGGAGTTCAAGACCAGCC 20020
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/note="Vector: DBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
RPCIII Human Male BAC Library"
31 c 29 g 22 t
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Pred. No. 1.3;
0; Mismatches
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Best Local Similarity
Matches 91; Conserv
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Other_GSSs: RPCIII-36G16.TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@titgr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
AQ046231 106 bp DNA GSS 14-APR-1999
RPCI11-36G16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-36G16,
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RPCI11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
TH: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
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Pred. No. 1.5;
0; Mismatches
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/db_xref="GDB:7513599"
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/clone_lib="RPCI-11"
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Job time: 508439 sec
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                                                                senomic survey sequence.
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AQ046231.1 GI:3315158
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Best Local Similarity 87.5%;
Matches 91; Conservative
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QY 20072 GCGTGGTGCTGCTGCTGTAATCCCAGCTACTCTGGAGGCTGAGGCA 20119

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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION A74.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 82.6; DB 4;
Pred. No. 2.5e-08;
PCT-US95-17111A-92
US-08-454-557C-91
US-08-410-426D-91
US-08-10-1711A-91
US-08-12-177A-166
US-08-12-177A-166
US-08-454-557C-60
US-08-450-673C-60
PCT-US95-17111A-60
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US-08-450-673C-69
US-08-450-673C-69
US-08-470-696-69
US-08-470-696-69
US-08-470-696-69
US-08-477-504A-66
US-08-477-504A-66
US-08-477-504A-66
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TILLE OF INVENTION: MN Gene and Protein
NUMBER OF SECUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STREET: California
                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATICN NUMBER: 30,863
REFERENCE/TOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-435-0234
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 US-08-481-658B-65/c
; Sequence 65, Aprilcation US/08481658B
: Patent No. 5955075
; GENERAL INFORMATION:
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LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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 RESULT
                                                                                  ; Search time 599.42 Seconds
(without alignments)
6288.907 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5E_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/ptogrus_comB.seq:*

7: /cgn2_6/ptodata/1/ina/packfiles1.seq:*

7: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-477-504A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-486-789-65
US-08-457-91
US-08-450-672-91
US-08-450-672-91
US-08-450-672-91
US-08-481-658B-65
US-08-486-756A-65
US-08-787-799-65
US-08-787-709-05
US-08-450-673C-70
US-08-440-426D-70
US-08-440-426D-70
US-08-440-426D-70
US-08-440-426D-70
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US-08-454-557C-92
US-08-340-426D-92
US-08-450-673C-92
                                                                                                                                    US-08-852-495C-2_COPX_168000_197000
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
                                                                                  June 20, 2000, 02:28:19
                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 110
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Database :

Result

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Sequence:

Run on:

Searched:

Length 105;

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Sequence 65, Application US/08486756A Patent No. 5981711
US-08-486-756A-65/c
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                                                                      Qy 18973 ATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTTTGAGACCAGC 19032
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   Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY-AGENT INFORMATION:
NAME: Lauder, Leona L.
RECISTRATION NUMBER: 30,863
RECISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
0; Mismatches 14; Indels
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                                                                                                                                                                                                              19033 CTGACCAACATGGTGAAACCCTGTCTCTACTAACAAATACAAAA 19077
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Pred. No. 2.5e-08;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-477-504A-65/c
; Sequence 65, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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86.78;
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LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 86.7
Matches 91; Conservative
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   Conservative
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CITY: Tiburon
STATE: California
COUNTRY: USA
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US-08-477-504A-65
91;
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   Matches
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RESULT

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QY 18973 ATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTTTGAGACCAGC 19032
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Pred. No. 2.5e-08;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAAA 1
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
              APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
ADDRESSE: Leona L. Lauder
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; Sequence 65, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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                                                                                                                                                                              6 Mariposa Court
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Best Local Similarity 86.7
Matches 91; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                  ZIP: 94920 ,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                            STREET: 6 Mariposa
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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GENERAL INFORMATION:
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US-08-486-756A-65
                                                                                                                                                                                                                                                 COUNTRY:
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US-08-454-557C-91/C
Sequence 91, Application US/08454557C
Sequence 10. 3830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1130 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18973 ATCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTTTGAGACCAGC 19032
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Pred. No. 2.5e-08;
0; Mismatches 14; Indels
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                                                                                                      PRICE ATTON DATA BY A PAPLICATION DATA BY A PAPLICATION NUMBER: US 08/485,049 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504 FILING DATE: 07-UN-1995 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658 FILING DATE: 07-UN-1995 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862 FILING DATE: 07-UN-1995 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862 FILING DATE: 07-UN-1995 PRIOR APPLICATION DATE: US 08/485,863 FILING DATE: 07-UN-1995 PRIOR APPLICATION NUMBER: US 08/485,863 FILING DATE: US 07-UN-1995 PRIOR APPLICATION NUMBER: US 08/485,863 FILING DATE: US 07-UN-1995 PRIOR APPLICATION NUMBER: US 08/487,077 FILING DATE: US 07-UN-1995 ATTORNEY AGENT INFORMATION:
ANAME: Landar Lan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-034
TELEPHONE: 415-981-033
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
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                                  FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.79
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COMPUTER READABLE FORM:
APPLICATION NUMBER:
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STATE: D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                     MEDION TYPE: KIOPPY disk

COMPUTER: Bur PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/477,504

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3D

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Bastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INFORTION:
TITLE OF INFORTION:
WABER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.7
Matches 91; Conservative
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STATE: California
                                      California
                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-787-739-65/c
                                                                                                                   94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-485-862B-65
                                  STATE: C. COUNTRY:
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Gaps

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Length 105;

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TYPE: nucleic acid
                                                                                                                                       both
                                                                                                STRANDEDNESS:
TOPOLOGY: bo
US-08-340-426D-91
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US-08-450-673C-91
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COMPUTRY: U.S.A.
2IP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET UNMBER: 36,203
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELEPHONE: CLOS) 371-2540
TELEPHONE: CLOS) 371-2540
INFORMATION FOR SEQ ID NO: 91:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGRWT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 371-2600
TELECOMMUNICATION SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs

"VER TENET AND TO THE TENET AND THE TENET
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STRANDEDNESS: both

TOPOLOGY: both

US-08-454-557C-91
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STATE: D.C.
COUNTRY: U.S.A.
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US-008-450-673C-91/c

Sequence 91, Application US/08450673C

Sequence 91, Application US/08450673C

Sequence 91, Application US/08450673C

Sequence 91, Application US/08450673C

GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.

TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Pox P.L.L.C.
                                                                                                      Qy 18963 CACGCCTGTAATCCCCAGCACTTTGGGAGGCCAAGGCGGACAGATCACGAGGTCAGGAGTT 19022
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Score 68.6; DB 4; Length 84;
Pred. No. 1.5e-05;
0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALUNESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
ATCASSIPICATION: 30
ATCASSIPICATION: 30
ATCASSIPICATION: SOFT
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 0609.3840004
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERICS:
                                                                                                                                                                                                      Qy 19023 TGAGACCAGCCTGACCAACATGG 19045
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       0.2%;
Query Match
Best Local Similarity 89.2%
Matches 74; Conservative
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STRANDEDNESS: both
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linear
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US-08-481-658B-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                              Ouery Match 0.2%; Score 68.6; DB 6; Best Local Similarity 89.2%; Pred. No. 1.5e-05; Matches 74; Conservative 0; Mismatches 9;
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US-08-481-658B-65
; Sequence 65, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: PRACTORENOW, SILVIA
APPLICANT: PRACTORENOW, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0609.3840002
RESULT 9
PCT-US95-17111A-91/c
; Sequence 91, Application PC/TUS9517111A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 19023 TGAGACCAGCCTGACCAACATGG 19045
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R.
REGISTRATION UNUBER: 36,203
REEFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 371-2600
TELEFAN: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDENESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CGACACCAGCCTGATGAACATGG 1
                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  both
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
PCT-US95-17111A-91
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27880 TTTTTATATTTTTAGTAGAGGGGGTTTCAGCATGTTGGTCAAGCTTGTCTCAAACTCC 27939
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURS YSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
RECISTRATION NUMBER: 30-0021.3E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 55:
SEQUENCE CHASACTERISTICS:
TENERAL 105 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY 27940 TGACCTCAGGTGATCCACCCACCTCGGCCTCCGAAAGTGTTG 27981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TGACCT--TGTGATCCACCTCGGCCTCCCAAAGTGCTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65.6; DB 4;
Pred. No. 6.9e-05;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 65, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; UNBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/477,504A FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.3%
"-+rhes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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0.2%; Score 65.6; DB 4; Length 105;
           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94920
                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-486-756A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-485-862B-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27880 ITITIATATITITAGIAGAGGGGTTTCAGCATGITGGTCAAGCTTGTCTCAAACTCC 27939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.C..
ZIP: 94930
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLOPPY STEM: PC-DOS/MS-DOS
SOFTWARE: PALCATION DATA: PC-DOS/MS-DOS
SOFTWARE: PALCATION DATA: PSPLICATION NUMBER: US/08/486,756A
FILING DATE: U7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
REGISTRATION NUMBER: 30,863
ATTORNEY CAGENT INCORMATION:
NAME: Lauder: Leona L.
REGISTRATION NUMBER: 30,863
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 65.6; DB 4; Length 105; 84.3%; Pred. No. 6.9e-05; tive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY 27940 TGACCTCAGGTGATCCACCTCGGCCTCCGAAAGTGTTG 27981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TGACCT--TGTGATCCACCACCACCTGGCCTCCCAAAGTGCTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Bastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INFORTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTONNEY, AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-435-034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STAATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.23
Best Local Similarity 84.3
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 base pairs
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US-08-477-504A-65
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QY 27880 TTTTATATTTTTAGTAGAGGGGTTTCAGCATGTTGGTCTAAGCTTGTCTCAAACTCC 27939
                                                                                                                                    0.2%; Score 65.6; DB 4; Length 105; ilarity 84.3%; Pred. No. 6.9e-05; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                           Qy 27940 IGACCTCAGGTGATCCACCACCTCGGCCTCCGAAAGTGTTG 27981

Db 62 IGACCT--TGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2334
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65, Application US/08485862B Patent No. 5989838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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14; Indels

Length 105;

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27880 TTTTTATATTTTTAGAGAGGGGTTTCAGCATGTTGGTCAAGCTTGTCTCAAACTCC 27939
                                                                                                                                                                                                                                    QY 27940 TGACCTCAGGTGATCCACCCACCTCGGCCTCCGAAAGTGTTG 27981
                                                                                                                                                                                                                                                                                                                                    62 TGACCT--TGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTG 101
                                                                                                  Query Match 0.2%; Score 65.6; DB 5; Best Local Similarity 84.3%; Pred. No. 6.9e-05; Matches 86; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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  ; ANTI-SENSE:
US-08-787-739-65
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                                                                             27880 TTTTTATATTTTTAGAGAGGGGTTTCAGCATGTTGGTCAAGCTTGTCTCAAACTCC 27939
                                                                                                                            2 TTTTTACATCTTTAGTAGAGACAGGGTTTCACCATATTGGCCAGGCTGCTCTCAAACTCC 61
                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/785-DOS
CURRENT APPLICATION DATA:

FILING DATE: US/08/787,739
FILING DATE: US/08/785,049
FILING DATE: US/08/486,756
FILING DATE: US/08/486,868
FILING DATE: US/08/486,868
FILING DATE: US/08/486,868
FILING DATE: US/08/485,868
FILING DATE: US/08/487,077
84.3%; Pred. No. 6.9e-05;
ive 0; Mismatches 14; Indels
                                                                                                                                                                          Qy 27940 TGACCTCAGGTGATCCACCCACCTCGGCCTCCGAAAGTGTTG 27981
                                                                                                                                                                                                       APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-787-739-65
: Sequence 65, Application US/08787739
: Patent No. 6027887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-(
TELECOMMUNICATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  Best Local Similarity 84.3
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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RESULT 15
US-08-222-177A-430
Sequence 430, Application US/08222177A
Sequence 430, Application US/08222177A
Sequence 430, Application US/08222177A
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewltt.Ross & Stevens, S.C.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
STATLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
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Pred. No. 0.00014;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Wisconsin
COUNTRY: USA
ZIP: 53177-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY-AGENT INPORMATION:
NAME: SATA, Charles S.
REGISTRATIÓN NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 09.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (608) 831-2100
(608) 831-2106
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Best Local Similarity 93.1%;
Matches 67; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 92 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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80 AACACACACACA 91

Search completed: June 20, 2000, 18:07:04 Job time: 537154 sec

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                                                                                                                                                                                                                                                 June 20, 2000, 17:56:59; search time 29135.9 Seconds (without alignments)
-601.018 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-852-495C-2_COPY_196000_214000
18001
1 CTARARAGIATITIRARACC......TGGACATGCTGTGTTCCTTC 18001
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 882769 seqs, -486395729 residues
                                                                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapoxt 1.0
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1: gb_bal:*

2: gb_bal:*

4: gb_on:*

5: gb_pal:*

7: gb_pl:*

7: gb_pl:*

9: gb_pl:*

10: gb_pl:*

10: gb_pl:*

10: gb_pr3:*

11: gb_pr3:*

12: gb_rc2:*

13: gb_rc3:*

13: gb_rc3:*

14: gb_pr3:*

15: gb_rc3:*

16: gb_rc3:*

17: gb_pr3:*

18: gb_rc3:*

18: gb_rc3:*

19: gb_rc3:*

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gb_htg1: *
gb_htg1: *
gb_htg2: *
gb_in1: *
gb_in2: *
em_ba1: *
em_ba2: *
em_bum3: *
em_bum
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em_sts:*
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em_un:*
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Maximum DB seq length: 110
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Sequence:
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                                                                                                                                                                     OM nucleic
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gb_htg7:*
em_htg1:*
em_htg2:*
em_htg3:*
em_hum5:*
gb_p13:*
gb_htg8:*
gb_htg8:*
gb_htg10:*
gb_htg10:*
gb_htg10:*
gb_htg11:*
gb_htg11:*
gb_htg11:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description		Нимап	3 Human	luman c	Human	8 Нишап	Human c	X05249 Human LDL-r	X05249 Human LDL-r	X05251 Human LDL-r	X05251 Human LDL-r	X57789 Human seque	4 Human	4 Human	Human	U67808 Human small	9 Human	Human	Human	Human	Human	7 Human			luman lo		G43535 WIAF-2393-S	M14180 Human low d	43 A009	Human	Humai	S79560 HRX (intron	Human 1	Human	Human			AF185109 Lastorhin	D16965 Human HepG2	L31299 Human STS U	-	Human	L30244 Human STS U	M14178 Human low d	M13479 Human alpha	48 Human
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Length DB		108	108	103	108	108	107	108	108	108	108	103	108	91	110	108	103	110	107	108	103	110	104	108	90	106	108	97	106	90	104	101	97	108	66	107	108	108	108	100	80	97	91	97	94	100
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-liopprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15729 CTTGGCTCATTGCAACCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGACTCAGCCTCCCG 15788
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Eukaryota, Metazoa, Chordata, Vertebrata, Mammalia, Eutheria,
Primates, Catarrhini, Hominidae, Homo
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M.A. and Deininger, P.L.
CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                     20-MAY-1992
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                                                                      Human LDL-receptor gene intron 14 fragment (normal gene)
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Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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0; Mismatches 11
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Human small cytoplasmic Alu transcript.
U67803
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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88.98;
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Matches 96; Conservative
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1 (bases 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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Pred. No. 2.3e-05;
0; Mismatches 6;
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 g 1
/rpt_family="Alu"
/rpt_type=dispersed
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Best Local Similarity 93.8%;
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M87924.1 GI:174871
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1 (bases 1 to 108)

1 (bases 1 to 108)

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
             Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. and Humphries, R. and Humphries, R. and Humphries, Independent crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL
density lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                        See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 0.00012;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                  Score 84; DB 10;
Pred. No. 8.4e-05
0; Mismatches 11
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87161901
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g 29 t
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23 c 39 g 18 t
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/organ1sm="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Alu repeat"</pre>
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38 c 20 g
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(bases 1 to 108)
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                                                                                                                                                                                                                                                                                                                                                 93; Conservative
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Best Local 9
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                AUTHORS
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QY 13476 TTGGCTCACTGCAACCTTTGCCTCTTGGGTTCAAGCAATTATCCTGCCTCAGCCTCCTTA 13535

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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukharyota, Metazoa, Chordata, Craniata, Vertebrata, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 107)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RRA transcripts in human embryonal carcinoma cells. Model opst-transcriptional selection of master sequences
J. Mol. 1992) In press
Location/Qualifiers
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61
                                                                                                                                                                                                                                                                               HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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                                                          Indels
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Pred. No. 0.00017;
0; Mismatches 13;
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87.4%; Pred. No. 0.
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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30 c 35 g 1
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48 GCAGGAAAATGGTTTGAACCCAGGAGGCAGAGGTTGTGGTGAGGCGA 2
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VERSION
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Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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Human LDL-receptor mutated gene with intron 12 deletion junction.
                                                                                                                                                                                                                                                        15730 TTGGCTCATTGCAACCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGACTCAGCCTCCCGA 15789
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                                                                                                                                                                                                                            Gaps
                                                                                                                     /note="deletion junction region intron 12/ intron 15" 40~{
m c} 20 g 28~{
m t}
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                                                                                                                                                                                               Length 108;
                                                                                                                                                                                                                                                                                                                 Qy 15790 GTAGCTGGGATTACAGGCATGCATCACCATGCCTGGGTAATTTTTGT 15836
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                                                                                                                                                                                                                            17; Indels
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                                                                                                                                                                                                                                                                                                                                62 GTAGCTGGGATTACAGGCACCTGCCACCACCACCACCTGGCTAATTTTTGT 108
of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES

Location/Qualifiers
                                                                                                                                                                                                DB 10;
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Pred. No. 0.00042;
0; Mismatches 17
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*source: hypercholesterol aemia
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Best Local Similarity 84.1%;
Matches 90; Conservative
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*Source: hypercholesterol aemia
See X0526 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
all-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNN.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Eukaryota, Matazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Williamson, R. and Humphries, I.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
Bru. J. Biochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                              Bukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarnhini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia BILL. J. Blochem. 164 (1), 77-81 (1987)
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1. .108
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
HSLDLRD2 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
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                                                                                                                                                                                Alu repetitive sequence; low density lipoprotein receptor.
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Pred. No. 0.00042;
0; Mismatches 17;
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20 c 40 g 20 t
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/organism="Homo sapiens"
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Best Local Similarity 84.1%;
Matches 90; Conservative
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COMMENT
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Genetic and physical mapping of simple sequence repeat containing
                 1716 CAAAACCAGCCTGGCCAACATGGTGAAAACCCATCTCTACT 1756
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Homo sapiens
                                                                                                                                                                                                                  Homo sapiens
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HSU67804/c
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ORIGIN
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AUTHORS
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AUTHORS
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KEYWORDS
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                 à
            In the defective LDL-receptor gene the deletion ocurred between two alu-repetifive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
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Submission (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler,R. Ralley,J.H., Ogilvie,D.J., Anand,R., Buxton,J.,
Davies,J., Johnson,K. and Markham,A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                        15730 TTGGCTCATTGCAACCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGACTCAGCCTCCCGA 15789
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
Aldridge,F.L.
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See X05250 for corresponding normal gene sequence
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Human sequence tagged site BICBR DNA from 19q13.
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Pred. No. 0.00054;
0; Mismatches 14;
                                                                                                                                                                                                                                                          Score 79.8; DB 10;
Pred. No. 0.00042;
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91367697
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/clone="8IC8"
28 c 23 a 22 t
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20 c 40 g 20 t
                                                                                                                                                                                                                                                                                            0; Mismatches
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/db_xref="taxon:9606"
/chromosome="19q13"
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ilarity 86.1%;
Conservative (
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1 Similarity 84.1%;
90; Conservative
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X57789.1 GI:23938
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HS8IC8R/c
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VERSION
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Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
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L30244.1 GI:605447
STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; tetranucleotide repeat.
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Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,
Melis, F., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy 15143 GTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 15202
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Shaikh, T.H., Roylor, Xim, J., Batzer, M.A. and Deininger, P.L.
cDNAs derived from primary and small cytoplasmic Alu (scalu)
                                                                                                                                                   01-AUG-1997
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
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42 CTTGACCAGCCTGGCCAACATGTGAAACCCTATCTTACT
                                                                                                                              HSU67804 108 bp RNA
Human small cytoplasmic Alu transcript.
U67804
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Pred. No. 0.00091;
0; Mismatches 11
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu3"
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/rpt_type=dispersed
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Best Local Similarity 87.6%;
Matches 85; Conservative 0
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Human STS UT8164, 5'
L30244
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Query Match
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SOURCE
ORGANISM
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HSU67808/c
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14965 TTTTTTTTTTTTTTTTTTGACTGAGTCTTGCTCTGTCTCACAGGCTGGAGTGCAGTGGTGCG 15024
             Unpublished (1994)
Submitted by: Utah Center for Human Genome Research University
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: ste@corona.med.utah.edu
Primer A: AGAGGTTGCAGTGAACCAA
Primer B: TTTTCCCCTCTTACTCACT
End to Label: Primer B
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 TTTTTTTTTTTTTTTGACAGAGTCTCACTGTCACCCAGGCTGGAGTGCAGTGGTG 32
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 110)
Shalkh, T. H., Roy, A. M., Klm, J., Batzer, M.A. and Deininger, P. L.
cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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                                                                                                                                                                                           Cycles Denaturation Annealing Extension 5 (10 sec. 56 C 10 sec. 72 C 20 sec. 30 94 52 C 10 sec. 72 C 20 sec. Mg++: 1.50 mM Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
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sequence tagged sites from the human genome
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Human small cytoplasmic Alu transcript.
U67807
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J. Mol. Biol. 271 (2), 222-234 (1997)
97415756
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/evidence=experimental
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/rpt_type=dispersed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
                                                                                                                              2 CCTGTAATCCCAGCACTTTGAGAGGCCAAAGTGGGTGGATCACTTGAGCCCAGGAGTTCA 61
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tive 0; Mismatches 13; Indels 0
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Direct Submission
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/organism="Homo sapiens"
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91 73 99 93 97 109 109		standard; DNA; 108 BP 1999 (first entry) ladder; HUMFIBRA/FGA 11946 1998; 305120. 1997; GB-013597. UN SEC STATE HOWE DE CD, Barber MD, Burker 1998; 305120. 1997; GB-013597. UN SEC STATE HOWE DE CD, Barber MD, Burker 1998; 305120. 1998. 1998; 305120. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998. 1998; 305120. 1998;	0.4%; larity 83.0%; Conservative	rcrircio 	FTTCTTTC 	standard; DNA; 108 BP 1999 (first entry) iallelic polymorphic phism; biallelic; hum
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New isolated nucleic acid segments from the human genome - used for New isolated nucleic forms for use in e.g. forensics, paternity determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
Claim 1: Page 219; 310pp; English.
X10269-X12937 are human DNA fragments which contain biallelic polymorphic
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Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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detection; phenotypic typing; characteristic; infection; hereditary;
                           auto1mmune disease; cancer; inflammation; drug; therapy; medicament;
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Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
Hudson T, Lander ES, Wang D;
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
                                                      treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 79; Conserv
                                                                               Homo sapiens.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9820165-A2.
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markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IURAC-IUB ambiguity code. These fragments can be used in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycysic Kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary sherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary sherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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double-stranded DNA, which comprises one of the 7837 "GS" sequences
given in 179001-126837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6421 TAATCCCAGCAC-TTTGGGAGGCCGAGGCAGGAGGATCACATGAGGTCAGAAATTCAAGA 6479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 TAATCCCAGCACTTTTGGGAGGCCAAGGCAGACGGATCACTTGAAGTCAGGAGTTCGAGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1996 (first entry)

Human gene signature HUMGS06998.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     macauara n, onuvo n;
WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 68.6; DB 1; Length 108; 33.8%; Pred. No. 0.055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 CCATCCTGGCCAACAYAGGAAAACCTCATCTATACAAAAAAGACA 1
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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Matches 14968

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Per Detection of polymorphic genetic markers of the form

Maris 37.042.297.04.

Famile 8; Coluum 57-58; 186pp; English.

Cd-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

Example 8; Coluum 57-58; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences

The invention relates to the isolation of polymorphic repeat sequences

C The invention relates to the isolation of polymorphic repeat sequences

CC markers. Primers based on these sequences can be used to detect these

CC markers. Primers based on these sequences can be used to detect these

CC commercial animal or plant breeding or pedigree analysis.

CC minan genetic analysis such as linkage analysis of genetic disease,

CC minan analysed, fall into 4 categories:

CC interruptions and without adjacent repeats of another sequence;

CC interruptions and without adjacent repeats of another sequence;

CC interruptions and without adjacent repeats of a sequence other than compound perfect repeats which are defined as 2 or more runs of at least

CC arepeats separated by no more than 3 consecutive non-repeat bases from a run of at least

CC dG-dA)n. (dG-dT)n, or from at least 10 uninterrupted mononuclectides; and

A) imperfect compound repeats which are defined as for the perfect

CC dG-dA)n. (dG-dT)n, or from at least 10 uninterrupted

A) imperfect compound repeats which are defined as for the perfect

CC onnound repeats sequence is an example of a compound imperfect repeat sequence of a compound interrupted.
18-JUN-1997 (first entry) (dC-dA)n.(dG-dT)n polymorphic repeat sequence #12.
Polymorphism: repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macsubara K, Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene signature HUMĠŚ06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 G;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure: T(CT)12GTT(TC)11T(CA)14A(AC)6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64;
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                                                                                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD CLINIC.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATE)/ MATESHBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                        21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
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WO9514772-A1.
                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using pridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
                                                                                                                                                                 8118 TTTCTTTTTCTTTCTGACAGGTCTTGCTCTATTGCCTAGGCTGGAGTGCAGTGGTGCAA 8177
                                                                                                                   Gaps
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                                                                                                                                                                                          100 TITGITICAAACAGAGTGTCACTCTGTCACCCAGGCNGGAGTGCAANGGTGCAATC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                  DB 1; Length 100;
                                                                                                                22; Indels
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                                                                                                                                                                                                                                                             15028 TCGCCTCACTGCAACCTCTGCCTCCCGGGTTCAAGTGAT 15066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 65.6; DB 77.8%; Pred. No. 0.14; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2029; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                   [26213 standard; cDNA to mRNA; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1996 (first entry)
Human gene signature HUMGS08452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1995.
11-NOV-1994; JO1916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K. Okubo K;
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T66081;
                                                                                                                   Conservative
                                                                                         Similarity
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                                                                                                              77;
                                                               Query Match
Best Local S
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RESULT 175 213/C 175 213/C 175 213/C 175 213/C 175 213/C 175 213 NW DT 13 NW DT 13 NW DT 17 N

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RESULT T66081 ID T

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Length 92; 5; Indels

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Sequence

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                                                                                                                                              A single-stranded DNA, which complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
c given in Tig001-T26837 and which is able to hybridise to part of
the mind of the Tig001-T26837 and which is able to hybridise to part of
the mind genomic DNA, cDNA or mank is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
to from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed as as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (ssp. using primers and probes derived from the GS
sequence) as a means of diagnosing abnormal cell function or for
crecognising different cell types.
Sequence 100 BP; 28 A; 22 C; 25 G; 27 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA mass initiated from the C from various human tissues; synthesis of CDNA was initiated from the 3'-and of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
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for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1893 CCTGGGTGACAGAGCAAGACTCCATTTAAAAAAAAAAA 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CCTGGGTGACAGAGTGACACTCTGTTTGAAACAAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T25009/C

ID T25009/C

AC T25009,

E Human gene signature HUMGS07131,

We can signature; messenger RNN, mRNA, rela

KW human; clondng; mapping; non-biased libra

Call typing; abnormal cell function; ss.

NO9514772-A1.

PR 12-NOV-1994; J01916.

PR 12-NOV-1994; J01916.

PR 12-NOV-1993; JP-355504.

PR (NCUBA) OKUBOR K.

PR (NCUBA) OKUBOR K.

PR (NCUBA) OKUBOR K.

PR (NCUBA) OKUBOR K.

PR (AMATS) MATSUBARA K.

PT (Calian 1: Page 1748; 2245pp; Japanese.

CC double-stranded DNA) which comprises one

CC double-stranded DNA) which comprises one

CC given in T19001-T25837 and which is able

CC given various human tissues; synthesis of

C in warious human tissues; synthesis of

C in than alaced sequence is unique to a part

CC all the 3'-oriented cDNAs hybridise with

CC The appearance frequency of a given GS in

C The appearance frequency of a given GS in

C The appearance frequency of a given GS in

C The appearance frequency of a given GS in

C The appearance frequency of a given GS in

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C The appearance frequency of a given GS in

C The appearance frequency of a given GS in

C The appearance frequency of a given GS in

C The appearance frequence coll the particular tissue
                                                                                                                     Claim 1; Page 1720; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 76.8 tes 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY 15182 GATCTCCTGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCAT 15241
                                                                                 17285 TTTGTTTGTTTGTTTTTTGAGATAGAGTCTTCCTCTGTCATTCAGGCTGGAGTGCAGTGG 17344
                                                                                                       107 TIGNIGITGITGITTTCAACAGGGTCTTGCTCTGTCACTCAGGCTGGAAINCAGTGG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATCTCCTGACCTCGTCATCCGCCCGTNTCGGCCTCCCATAGTGCTGGGNTTACAGGCAT 60
                                                                                                                                                                                                                                                                                                                                      126828;
14-NOV-1996 (first entry)
14-Nov-1996 (first entry)
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 63.8; DB 1; Length 108; 88.3%; Pred. No. 0.26; 1ve 0; Mismatches 9; Indels
Length 108;
                                                                                                                                                                 Qy 17345 CATGATCTCAGCTCACTGCAGCCTCCGCCTCCCGGGTTCAAGAGAT 17390
                                        27; Indels
                                                                                                                                                                                        Score 64; DB 1;
Pred. No. 0.24;
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                 T26828 standard; cDNA to mRNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V11611/c
ID V11611 standard; cDNA; 106 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 15242 GGGCCACCACGCCTGGC 15258
  0.48;
Query Match
Best Local Similarity 74.5
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 88.3
les 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAGCCACCACGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 95-206931/27
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Query Match
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                                                                                                                                                                                                               Worlesto actus encoung nover secrete protests as userul as, e.g. anti-inflammatory, immuno-stimulatory or suppressing agents claim 30; Page 73; 110pp; English.

The sequence is that of an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or ameliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers for tissues, molecular weight markers for gels, primers or probes, for nutrition as carbon, nitrogen or carbohydrate source. They can also be used as a cytokine for cell proliferation and differentiation activity, as immune stimulants or suppressors, e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systemic lupus erythematosus, to regulate haematopoiesis, for tissue growth, as an activator or inhibitor, or as a chemotactic or chemokinetic, haemostatic and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitor agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1748; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1996 (first entry)
Human gene signature HUMGS07131.
Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                        Homo sapiens adult retina clone B0365_2 3' region.
adult; retina; cDNA library; clone B0365_2; anti-inflammatory;
therapeutic composition; autoimmune disease; immune; stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding novel secreted proteins - useful as, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.3%; Score 62.8; DB 1; Length 106; 74.5%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agostino MJ, Jacobs K, Lavallie ER, Mccoy JM, Merberg D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.36
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T25009 standard; cDNA to mRNA; 108 BP
                                                                                                                                                                             Racie LA, Spaulding V, Treacy M; WPI; 98-240082/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                  104 A;
                                                                                                                      03-OCT-1997; U18007.
04-OCT-1996; US-726237.
(GEMY) GENETICS INST INC.
           11-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 74.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okubo K;
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                                                                                            WO9814576-A2.
09-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                  Homo sapiens
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numan genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cc all the 3'-oriented copus hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular rissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be constructed so as an eans of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1833 ATCACTTGAACTCAGGAGGCAGAGGTTGTAGTGAGCTGAGATCGCACCACTGCACTCCAG 1892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T1901-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented CDNA hybridise with specific mRNAs. Bach library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ATCCCTGAGCCCATGAGGCCAAGGCTGCAGTGAGCCATGGTCACGCCACTGNATTCCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Human gene signature HUMGS08084.

Human gene signature; messenger RNA: mRNA; relative abundance; frequency; human; cloning; messenger RNA: mRNA; mRNA; diagnosis; detection; cell typing; abnormal cell function; ss.

WO95147,2-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.3%; Score 62.4; DB 1; Length 108; 73.6%; Pred. No. 0.41; tive 0; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CCTGAGTGACAGAGCCCTGTTGAAAACAACAACAACAACANCAA 107
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Best Local Similarity 77.5
Matches 69; Conservative
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Matches 78; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSÜBARA K.
(OKUB/) OKUBO K.
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Okubo K;
            WPI; 95-206931/27.
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WO9514772-A1.
Matsubara K,
                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                   tissues
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                                                                                                                                                                                                                                                                                                                                                                               PT Octation of polymorphic genetic markers of the form

(dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

(dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

Disclosure; Column 1-12; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences

narkers. Primers based on these sequences can be used as genetic

markers. Primers based on these sequences can be used to detect these

commercial animal or plant breading or pedigree analysis clones

commercial animal or plant breading or pedigree analysis. Clones

containing the repeat sequences were isolated by hybridisation of

chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT)

probe. Over 100 repeat blocks were isolated. The inserts from the clones

were amplified by primers 165798-166047. Those clones where the repeat

sequence has been determined are shown in 165704-797. This repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                      17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd67.
Repeat sequence from polymorphic marker; primer; amplification;
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR: polymerase chain reaction; paternity; maternity; human; pedigree;
Innkage analysis; genetic disease; animal; plant; breeding; locus;
hybridisation; chromosome; ds.
1833 ATCACTTGAACTCAGGAGGCAGAGGTTGTAGTGAGCTGAGATCGCACCACTGCACTCCAG 1892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ATCACTTGAGCCTAGGAGGCAGNGGTTCAAGTGAGCTGAGATGGCACTCCTGCGCTCCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1996 (first entry)

Human gene signature HUMGS02180.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

HOMO Saplens.

W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.3%; Score 59; DB 1; Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence having the formula: (TC)12(AC)18.
Sequence 60 BP; 18 A; 30 C; 0 C
                                                    1893 CCTGGGTGACAGACAAGACTCCATTTAA 1921
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                                                                              CCINGGIGACAGCGIGAGANNCIGICICA 90
                                                                                                                                             T65762 standard; DNA; 60 BP.
                                                                                                                                                                                                                                                                                                                                              (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                            10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.3
Best Local Similarity 100.
Matches 59; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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US5582979-A.
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Claim 1; Page 758-759; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNAs in almost is constructed so as to reflect accurately the relative abundance of its constructed so as to reflect accurately the relative abundance of different mRNAs, in the particular rissue from which it was derived. The appearance frequency of a given GS in a cDNA library determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 22 A; 21 G; 21 G; 31 T;
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA libraries prepared and man tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be
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MPI: 95-206931/27
Identifying gene signatures in 3'-directed human cDNA library - e.g.
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                  e.9
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identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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0; Mismatches
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ID T21566 standard; cDNA to mRNA; 87 BP.
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03-AUG-1996 (first entry)
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LLNL; conta IMAGE Consortium (info@image.llnl.gov) for further inform Insert Length: 1127 Std Error: 0.00 Seq primer: -41ml3 fwd. Er from Amersham High quality sequence stop: 102. FEATURES Location/Qualifiers		3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	15194	AA703692 AA703692 106 bp mRNA EST 24-DEC- LOCUS AA703692 106 bp mRNA EST 24-DEC- DEFINITION ag81a10.r1 Stratagene hNT neuron (#937233) Homo sapiens of IMAGE:1140858 5' similar to contains Alu repetitive eleme Sequence. ACCESSION AA703692.1 GI:2713610 KEYWORDS AA703692.1 GI:2713610 KEYWORDS EST. SOURCE Human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma	Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE I (Dases 1 to 106)  Hillari.L., Allen, W. Bowles, L., Dubuque, T., Geisel, G., J. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M. Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, Washon Worl human ESP project JOURNAL Onpublished (1997)  COMMENT On Sep 12, 1996 this sequence version replaced g1:1397630  CONTACT: Wilson RK Washington University School of Medicine  4444 Forest park Parkway, Box 8501, St. Louis, NO 63108  Tel: 314 286 1810  Fax: 314 286 1810  Email: estewatson. wustl.edu This clone is available royalty free through LLNL; conta
AA243009 ZZ25h02.s AA703692 ag81a10.r AA55533 nk42b11.s B48914 RPCI11.4A12 AQ386882 RPCI11-13 AQ535244 RPCI-11-3 AQ544957 CITBI-E1- B17434 345K2.TVB C AA89736 am065h02.s	AA244245 nc07a04:s AA244245 nc07a04:s AA05553 nc47211-1D AA55553 nc47211-11 AQ053722 RPCT-11-4 AQ0363724 RPCT-11-4 AQ036349 CIT-HSP-2 AA250812 zo06a05:s B17434 345K2.TVB C AA564562 nt75£0.s AQ264176 CITBI-EI-AQ265749 CITBI-EI-AA583252 nn41e04:s	AQ05990 RPCI11-41 AQ0592186 RPCI-11-4 A1991750 W448e01.x A1991750 W448e01.x H67040 Yu686001.x1 B48088 RPCI11-4N6. AQ544583 CITBL E1- AA554869 no21e02.s AA078003 7H12D08 C AQ0540182 CIT-H5P-2	B32951 HS-1016-A1- AQ200347 RPCT11-43 AA570438 nk63902.s AQ534922 RPCT-11-3 B15423 345B10.TV C AA812141 0048B02.s N25299 V952C09.s1 AA250812 zs0605.s	AQ26242 CITBL-188-2 AQ265749 CITBL-E1- AA837701 0e06c02.s EST 11-MAR-1998 ccursor 937230 Homo sapiens	contains Alu repetitive .ve element; mRNA sequence. ; Vertebrata; Mammalia; .dae; Homo. lue,T., Geisel,G., Jost,S., Lennon,G., Marra,M., Steptoe,M., Tan,F., ston,R. and Wilson,R.
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1.1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone clu40858 5' similar to contains Alu repetitive element;, mRNA
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'id, M. More, B., Schellenberg, K., Steptoe, M., Tan, F.,
'id, Monte, Y., Wylie, T., Waterston, R. and Wilson, R.
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orest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                               /db_xref="taxon:Stprens"/db_xref="taxon:Stprens"/db_xref="taxon:Stprens"/db_xref="taxon:Stock"/db.xref="taxon:Stock"/db.xref="taxon:Stock"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/dev_stage="hwr neurons"/db_northigh="hwr neurons"/db.yref="hwr 
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Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Con Sep 12, 1996 this sequence version replaced gi:1393355.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nk42bl1.s1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1016157 3' similar to contains Alu repetitive element;, mRNA sequence. AA565533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15137 TTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCG 15196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. [ (bases 1 to 107) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.097;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy 15197 TGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 15242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGATCTGCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTG 106
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifilers
       primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ww-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1016157"
Seq primer: 28m13 rev. High quality sequence stop: 53.
Location/Qualifiers
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

E Lobasa 1 to 103)

S Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Mible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)

L Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.mac.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B48914 103 bp DNA GSS 08-APR-1999
RPCIII-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12,
genomic survey sequence.
B48914 GI:2601151
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 28 c 30 g 15 t
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tive 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:7501163"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11"
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Matches 97; Conservative
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DB 84; Length 103;

0.5%; Score 90.2;

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Class: BAC ends
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AQ386882
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Fleter de Jong
(pleter@deJong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                    AQ386882 110 bp DNA GSS 21-MAY-1999
RPCIII-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
genomic survey sequence.
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Venter. J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
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                                                      15133 TGTATTTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCCTGAC 15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
26 c 38 g 20 t
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                                                                        103 TGTATTTTTAGTAGAGAGGGGTTTCACCGTTTTAGCCGGGATGGTCTCGATCTCTGAC 44
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Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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0.14;
ches 10; Indels
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Other_GSSs: RPCIll-13414.TJ
Other_GSSs: RPCIll-13414.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
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                  8; Indels
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 Pred. No. 0.14;
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Pred. No. 0.14;
0; Mismatches
                0; Mismatches
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/clone_lib="RPCI-11"
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92.28;
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Matches 96; Conservative
                  95; Conservative
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Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Mams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

Gontear: Shaying Zhao, William Nierman, Mark Adams

Contear: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pleter@dejong.med.buffalo.edu). Clones may be purchased from

Research Genet cs (http://Dacpac.med.buffalo.edu/ordering) or from

Research Genet cs (http://Dacpac.med.buffalo.end.ordering) or from

Research Genet cs (http://Dacpac.med.buffalo.end.search/bac_end_search.html.

Seq primer: Tr.

Class: har ord
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RPCII1-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
17 c 27 g 18 t
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AQ535244 103 bp DNA GSS 18-
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
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                                                          RPCI-11-317H22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 88.6; DB
llarity 91.3%; Pred. No. 0.22;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="cob:761533"
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/clone="rexor:11-317H22"
/clone="lb="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .103
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence. AQ386882
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                                                                                                                 AQ535244.1 GI:4846934
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE AUTHORS

TITLE

JOURNAL COMMENT

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Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.

Jacob and J. M. Rounsley, S.R. and Venter, J.C.

Use of a BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1997)

Other GSSs: 345K02. TP 345K02. TPB

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org
Clones are available from Research Genetics (Info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                         Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3.21
Class: BAC ends.
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345K2.TVB CIT978SKA1 Homo sapiens genomic clone A-345K02, genomic
survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"CITBI-El"
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CalTech Human BAC Library D"
a 26 c 36 9 18 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15155 TTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCGGCCTCGGC 15214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 TITCACCEGETIAGCCAGAAIGGICTIGATCTCCTGACCTAATGATCTGCCCGCCTGGC 47
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87.4; DB 108;
Pred. No. 0.29;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                    Location/Qualifiers
1.106
//Organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                        Fax: 301 838 0208
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ORGANISM
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TITLE
JOURNAL
COMMENT
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Butaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia;
Butheria: Frimantes; Catarrhini; Hominidae: Homo.

Butheria: Frimantes; Catarrhini; Hominidae: Homo.

E 1 (bases 1 to 106)

Z hao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Bullding

Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850
                                    E 1 (bases 1 to 110)
S Lhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.(C.)
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
L Unpublished (1997)
Coher_GSSS: RPCII1-13414.TJ
Coher_GSSS: RPCIII-13414.TJ
Coher_GSS: RPCIIII-13414.TJ
Coher_GSS: RPCIII-13414.TJ
Coher_GSS: RPCIII-13414.TJ
Coher_GSS: RPCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tmgr.org/tdb/humgen/bac_end_search/bac_end_search.html
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
38 q 20 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10375 GGCCGGGCCTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGCAGGCTGAGGCGGGCAGA 10434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQS44957 106 bp DNA GSS 28-MAY-1999
CITBI-E1-2629N2.TF CITBI-E1 Homo sapiens genomic clone 2629N2.
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Pred. No. 0.27;
0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
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Best Local Similarity 87.3%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: T7
Class: BAC ends.
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

LOCUS DEFINITION AQ544957/c

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ACCESSION

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Gaps

source

FEATURES

BASE COUNT ORIGIN

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LE (Dases 1 to 103)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151346.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nlh.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CONG distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNI.at:

www-blo.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86.6; DB 38; Length 103;
Pred. No. 0.37;
0; Mismatches 9; Indels 0
                                                                                         QY 15197 TGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 15242
                                                                                                                      Qy 15202 CACCGGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATG 15242
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
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AA807640.1 GI:2877108
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91.1%;
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/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH119W, testis NHT, and B-cell
NCL_GAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682652-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Un Jan 19, 1998 this sequence version replaced gi:2150764.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov.
This clone is available royalty-free through Lini.; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 834 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality: sequence stop: 63.
Location/Qualifiers
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                                                                                                                                                   DB 84; Length 109;
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1 30 c 31 g 24 t
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                                                                                                                                                Score 87.2; DE
Pred. No. 0.3;
0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:1466067"
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AA244245

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VERSION KEYWORDS

ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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Homo sapiens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pieter do Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Kesearch Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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RPCI11-1D10.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1D10,
                                                                                                                                                                                                                                                                                                                                      Use of BAC End Sequences for Sequence-Ready Map Building (1998) Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mdadams@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC
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Pred. No. 0.36;
0; Mismatches 14;
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/organism="Homo sapiens"
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AA565533.1 GI:2337172
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AQ003188.1 GI:3030392
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 110)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I Onpublished (1997)

On Jan 24, 1995 this sequence version replaced gi:634306.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberg@hih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CONA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CONA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //note="Vector: pawpl0; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pawPl0 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krisman." I others
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                                                                       AA244245 110 bp mRNA EST 20-AUG-1997 nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1999
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86.4%; Pred. No. 0.36;
tive 0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1007406"
/clone_lib="NCI_CGAP_Pr1"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .110
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AA244245.1 GI:1875104
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FEATURES

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BASE COUNT ORIGIN

Matches

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Search completed: June 20, 2000, 09:51:36
Job time: 508463 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InActs:1016157"
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xhol; Cloned unidirectionally. Primer: Oligo dT. Bulk
germ cell tumor. 5' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'
Average insert size: 1.2 kb."
22 a 34 c 26 g 25 t
                                                                                                                                                                                                                               Fig. 1.

Clone distribution: WCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Building
          Townsol Towns Annual Sequence version replaced g1:1393355.
On Sep 12, 1996 this sequence version replaced g1:1393355.
Contact: Robert Strausberg, Ph.D.
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael i Emmert-Buck, M.D., Ph.D.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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87.9%; Pred. No. 0.4;
Live 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6603 GGGAGGCAGAGATTGCAATGAGCTGAGATCATGCCACTGCACTCCAG 6649
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9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 GGGAGGCAGAGCTTGCAGTGAGCTGAGATTGAGCCACTGCACTCCAG 1
                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 1661 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 87. Location/Qualifiers
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Contact: Mark Adams
Department of Eukaryotic Genomics
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B65160.1 GI:2639138
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Best Local Similarity 87.9
Matches 94; Conservative
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Tumor Gene Index
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Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                  /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
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                                                                                                                                                                                                                             /clone="2017G2
                                                                                                                                                                                                                                                                     /sex="Male"
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ALIGNMENTS

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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
                                                                                                                                                                                                                                                                            Sequence 65. Application US/08481658B
Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TORNEY/Aben, ....
NAME: Lauder, Leona L.
REGISTRATION UNBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/481,658B FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/260,190 FILING DATE: 15-JUN-1994 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-481-658B-65
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0000000000000
                                                                       June 20, 2000, 18:07:04; Search time 599.42 Seconds (without alignments) 3903.542 Million cell updates/sec
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18001
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-481-6588-65
US-08-485-7564-65
US-08-485-8628-65
US-08-787-739-65
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US-08-450-673C-91
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US-08-454-557C-91
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US-08-486-756A-65
US-08-485-862B-65
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 110
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Length 105;

Score 78.4; DB 4; Pred. No. 6.9e-09;

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US-08-486-756A-65
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                                            15129 TTTTTGTATTTTTAGTAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCC 15188
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  Gaps
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                                                                   2 TITITACATCITIAGTAGAGACAGGGTITCACCATATIGGCCAGGCTGCTCTCAAACTCC 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY,AGENT INFORMATION:
NAME: LAUGHEY, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Indels
  16; Indels
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                                                                                                                                     15189 TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGAT 15232
                                                                                                                                                            62 TGACCTTGTGATCCACCACCTCGCCTCCCAAAGTGCTGGGAT 105
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Pred. No. 6.9e-09;
0; Mismatches 16;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            Sequence 65, Application US/08477504A Patent No. 5972353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Leona L. Lauder
6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.4%;
Best Local Similarity 84.6%;
Matches 88; Conservative
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88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6 Maripose
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-477-504A-65
                                                                                                                                                                                                                                                  RESULT 2
US-08-477-504A-65
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  Matches
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QY 15129 TTTTTGTATTTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCC 15188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/486,756A
FILING DATE: 07-UNN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 15189 TGACCTCGTGATCCACCGGCCTCGGCCTCCCAAAGTGCTGGGAT 15232
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                        APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-0021.3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 65, Application US/08485862B
Patent No. 5989838
GENERAL INFORMATION:
Sequence 65, Application US/08486756A Patent No. 5981711 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                       STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                           CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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RESULT

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APPLICATION NUMBER: US/08/787,739 FILING DATE: 24-JAN-1997 PRIOR APPLICATION DATA:
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US-08-787-739-65
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                                                                                                                                                                                                                               OPERATING SISTEM: PC-LUS/MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFTCATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRICKATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3D
FILECOMMUNICATION NUMBER: D-0021.3D
FILECOMMUNICATION NUMBER: D-0021.3D
FELECOMMUNICATION NUMBER: S-0021.3D
FELECOMMUNICATION NUMBER: S-0021.3D
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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Fatent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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CITY: San Francisco
STATE: California
COUNTRY: USA
                                       California
                                                                 USA
                                                                                                  94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
US-08-485-862B-65
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US-08-787-739-65
                                    STATE: C
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15129 TTTTTGTATTTTTAGTAGAGATGGAGTTTCGCCGTGTTAGCCAGGATGGTCTCGATCTCC 15188
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Pred. No. 6.9e-09;
0; Mismatches 16; Indels
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Sequence 65, Application US/08481658B
Fatent No. 5955075
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION UNBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRICH DATE: 07-JUN-1995
PRICH DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
PRICH DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                          PALLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-0021.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-981-0332 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-981-0332
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Best Local Similarity
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Qy 10402 ATCCCAGCACTTTGGCAGGCTGAGGCGGGCAGATCACTTGAGGTCAGGAGTTTGAGACCA 10461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 72.8; DB 4; Length 105; 86.8%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 10462 GCCTGGCCAACATGGTGAAACCCTGTCTCCACTAAAAATACAAAA 10507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 GCCTGGCCAATATGGTGAAACCCTGTCTACTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
                           REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/486,756A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-486-756A-65/c
'Sequence 65, Application US/08486756A
'Patent No. 5981711
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPENATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%
Best Local Similarity 86.8%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGATGATCAC--AAGGTCAGGAGTTTGAGAGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 72.8; DB 4; Length 105; 86.8%; Pred. No. 1.2e-07; ative 0; Mismatches 12; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10462 GCCTGGCCAACATGGTGAAACCCTGTCTCCACTAAAATACAAAA 10507
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 GCCTGGCCAATATGGTGAAACCCTGTCTTATAAAAA 2
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Sequence 65, Application US/08477504A

Sequence 65, Application US/08477504A

PREMAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastcrekova, Silvia
STREBT: Galifornia
STATE: California
STATE: USA
                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPRAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEO 1D NO: 65 SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-481-658B-65
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10402 ATCCCAGCACTTTGGCAGGCTGAGGCGGCAGATCACTTGAGGTCAGGAGTTTGAGACCA 10461
                              105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGATGATCAC--AAGGTCAGAGTTTGAGAGCA 48
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION NUMBER: US 08/486,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,566
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: LANGAT INFORMATION:
                                                                                                   Qy 10462 GCCTGGCCAACATGGTGAAACCCTGTCTCCACTAAAAATACAAAAA 10507
                                                                                                                          47 GCCTGGCCAATATGGTGAAACCCTGTCTTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: My Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Sulte 610
CITY: San Francisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: D-0021.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         RESULT 10
US-08-787-739-65/c
: Sequence 65, Application US/08787739
: Patent No. 6027887
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                         105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGATCAC--AAGGTCAGAGTTTGAGAGCA 48
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                                                                                                                                            0.4%; Score 72.8; DB 4; Length 105; 86.8%; Pred. No. 1.2e-07; Live 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              QY 10462 GCCTGGCCAACATGGTGAAACCCTGTCTCCACTAAAAATACAAAAA 10507
                                                                                                                                                                                                                                                                                                                                                                          47 GCCTGGCCAATATGGTGAAACCCTGTCTACTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-0021.3D
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-00-485-862B-65/c
; Sequence 55, Application US/08485862B
; Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                            Query Match
Best Local Similarity 86.8%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 86.8
Matches 92; Conservative
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                         ; HYPOTHETICAL:
; ANTI-SENSE: N
US-08-486-756A-65
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US-08-485-862B-65
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US-08-454-557C-91
      IS-08-454-557C-91
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
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                                                                                   10402 ATCCCAGCACTTTGGCAGGCTGAGGCGGCCAGATCACTTGAGGGTTTGAGACCA 10461
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      Length 105;
                                                                                                                                                               10462 GCCTGGCCAACATGGTGAAACCCTGTCTCCACTAAAATACAAAA 10507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 64; DB 1; Length 92; 93.1%; Pred. No. 1.1e-05; tive 0; Mismatches 5; Indels
                                              12; Indels
                                                                                                                                                                                                         47 GCCTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
    0.4%; Score 72.8; DB 5;
86.8%; Pred. No. 1.2e-07;
tive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATE:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTONEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEPHONE: (608) 831-2106
                                                                                                                                                                                                                                                                                                   Sequence 430, Application US/08222177A Patent No. 5582979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIE: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 430:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-222-177A-430
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Best Local Similarity 93.19
Matches 67; Conservative
Query Match 0.4
Best Local Similarity 86.8
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 92 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 CACACACACA 219
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Sequence 91, Application US/08454557C

Patent No. 5830670

GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 91, Application US/08340426D
Patent No. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Dela Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 15160 CCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCGGCCTCGGCCTCCC 15219
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OY 15220 AAAGTGCTGGGATTACAGGCATG 15242
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 71; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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ZIP: 20005-3934
COMPUTER READABLE FORM:
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Gaps

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Length 84;

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Qy 15160 CCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCGGCCTCGGCCTCCC 15219
                                                                                                                                                                                                                                                                           Sequence 91, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT de la Monte, Suzanne
APPLICANT de la Monte, Suzanne
APPLICANT Neurol Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                 0.4%; Score 63.8; DB 4; Length 84
85.5%; Pred. No. 1.1e-05;
tive 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILLING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                 Query Match 0.4%
Best Local Similarity 85.5%
Matches 71; Conservative
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Best Local Similarity 85.59
Matches 71, Conservative
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TYPE: nucleic acid
              nucleic acid
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                                  ; STRANDEDNESS: b
; TOPOLOGY: both
US-08-450-673C-91
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CLASSIFICATION:
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PCT-US95-17111A-91
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APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TILE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 15160 CCGTGTTAGCCAGGATGCTCTCGATCTCCTGACCTCGTGATCCACCGGCCTCGCCTCCC 15219
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: BLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGBNT INFORMATION:
NAME: Ludwig, Steven R:
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUIENCE CHARACTERISTICS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Ludayl, Steven R.
REGISTRATION NUMBER: 0609.3840002
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-240
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Pred. No. 1.1e-05;
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Patent No. 5948888
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Best Local Similarity 85.5%;
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US-08-450-673C-91
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Qy 15160 CCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCGGCCTCGGCCTCCC 15219
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  Length 84;
0.4%; Score 63.8; DB 6; Length 8.85.5%; Pred. No. 1.1e-05;
Live 0; Mismatches 12; Indels
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61 AAAGTGCTGGGATTACAAGCGTG 83

Search completed: June 20, 2000, 18:07:26 Job time: 537176 sec

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0.3
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 110
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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AUTHORS
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AUTHORS
TITLE
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MEDLINE
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1 (Dases I to 108)

Horstemake, B.; Beisiegel, U., Dunning, A.; Havinga, J.R.; Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
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1 (bases 1 to 107)

2 Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                             20-MAY-1992
                                                                                                         Alu repetitive sequence; low density lipoprotein receptor
                                           HSLDLRN2 108 bp DNA PRI 20-MAY
Human LDL-receptor gene intron 14 fragment (normal gene)
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Pred. No. 1.9e-05;
0; Mismatches 6; Indels 0
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Homo sapiens male embryo carcinoma CDNA to other RNA
Homo sapiens
                                                                                                                                                                                                                                                                                                                See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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23 c 39 g 18 t
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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/db_xref="taxon:9606"
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87161901
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AUTHORS
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Eukaryoter, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 108)

1 (chases 1 to 108)

1 (chases 1 to 108)

Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Fur. J. Biochem. 164 (1), 77-81 (1987)

87161901

See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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                                                                                                                   Qy 14072 TTTTGAGACGGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGCCGGTCTCGGCT 14131
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                                                               Gaps
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                                                                                                                                                    16 TITITGAGACGGAGTCTCGCTCTCGCCCAGGCTGGAGTGCAGGCGCGCATCTCGGCT 47
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1 (bases 1 to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alu repetitive sequence; low density lipoprotein receptor.
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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      Length 107;
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                                                            Indels
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                                                                                                                                                                                                                                                                     46 CACTGCAAGCTCCCGCGTTCACGCCATTCTTCTGCC 5
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11arity 89.8%; Pred. No. 0.00028;
Conservative 0; Mismatches 11;
Score 90.8; DB 9;
Pred. No. 0.00025;
0; Mismatches 7;
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Human small cytoplasmic Alu transcript.
U67803
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23 c 39 g 18 t
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/db_xref="taxon:9606"
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   0.48;
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                              Best Local Similarity 93.1
Matches 95; Conservative
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HSLDLRD2/c
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See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion curred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Williamson, R. and Humphries, S.
Unequal crossing-over between two alurepetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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            2 (bases 1 to 108)
Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Direct Submission
Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
1. 108
//Organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="TscAlu2"
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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Primates; Catarrhini; Hominidae; Homo.
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Alu repetitive sequence; low density lipoprotein receptor
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Pred. No. 0.00037;
0; Mismatches 4;
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Pred. No. 0.00067;
0; Mismatches 12;
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/rpt_type=dispersed
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88.8%;
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Best Local Similarity 95.8°
warches 92; Conservative
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Best Local Similarity 88.8
Matches 95; Conservative
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*Source: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lioprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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                                                                                                                                                                                                                                                                                                                                                                       Human LDL-receptor mutated gene with intron 14 deletion junction.
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16884 TIGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTTCCAA 16943
                                2 TCGCCTCACCACAACCTCTGCCTCCTGGGTTCAAACCATTTTCCTGCCTCAGCCTCCCGGA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke,B., Beisiegel,U., Dunning,A., Havinga,J.R.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       Qy 16944 GTAGCTGGGATTACAGGCACCCACTACCACGCCTGGCTAATTTTTGT 16990
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
                                                                                                                                                        GTAGCTGGGATTACAGGCACCTGCCACCACCACGCCTGGCTAATTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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Pred. No. 0.00067
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20 c 40 g 20 t
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Best Local Similarity 88.8%;
                                                                                                                                                                                                                                                                                                                                          108 bp
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M87896.1 GI:174874
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X05249.1 GI:34335
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87161901
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KEYWORDS
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SOURCE
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ACCESSION
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                                                                                                                                                                                                                                                                                                  14105 CTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCCGGCTTCCAGGGTTCAAGTGAT 14164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotzi Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104).

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                    103 CTGGAGTGCAATGGCACGATCTCGGCTCACTGCAACCTCCCGCCTCCCGGGTTCAAGCGAT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Alu RNA transcripts in human embryonal carcinoma cells. Model
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Human carcinoma cell-derived Alu RNA transcript, clone CE272.
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Pred. No. 0.0042;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                     Length 103;
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Homo sapiens male embryo carcinoma cDNA to other RNA
Homo sapiens
              post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press Location/Qualifiers
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                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                  0.4%; Score 87.2; DB 9;
92.0%; Pred. No. 0.00083;
tive 0; Mismatches 8;
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                                                           1. 103
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Wrera2D1"
/dev_stage="embryo"
                                                                                                                                                   /tissue_type="carcinoma"
27 c 33 q 1
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26 c 37 q 1
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/cell_line="NTera2D1"
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Best Local Similarity 89.0%;
Matches 89; Conservative
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                                                                                                                                        /sex="male"
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Matches 92; Conservative
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HUMALCE272/c
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VERSION
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TITLE
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Solution.
Solution: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                see X05248 for corresponding normal gene sequence In the defective LDL receptor gene the deletion courred between two allurepetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame
                                                                                                    Eukaryotra, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 108)

1 (bases I to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia for Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotta; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)

1 (bases 1 to 108)

1 (bases 1 to 108)

Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia for Eur.

5 Euchem. 164 (1), 77-81 (1987)
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7243 ACAAAAATTAGCCAGGTGTGGTGGCAGGCACCTGTAATCCCAGCTATTCAGGAGGCTGAG 7302
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Alu repetitive sequence; low density lipoprotein receptor.
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0.3%; Score 81.4; DB 10; Length 108;
Best Local Similarity 85.0%; Pred. No. 0.0058;
Matches 91; Conservative 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7303 ACAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCATTGAGCCAA 7349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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15-APR-1994

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Butharia, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 107).

1 (bases 1 to 107).

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences

J. Mol. Biol. (1992) in press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcription in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences

J. Mol. Biol. (1992) In press

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7302 GACAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCATTGAGCCAAGATCATGCCACT 7361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7273 CCTGTAATCCCAGCTATTCAGGAGGCTGAGACAGGAGAATCGCTTGAACCCAGGAGGTGG 7332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GGCAGAAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCACT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
               HUMALCE162 107 bp ss-RNA
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
                                                                                                         Homo sapiens male embryo carcinoma cDNA to other RNA Homo sapiens
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Pred. No. 0.014;
0; Mismatches 12; Indels
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Pred. No. 0.011;
0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="carcinoma"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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27 c 33 g 1
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/sex="male"
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Best Local Similarity 87.8%;
Matches 86; Conservative
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                                                                     M87924.1 GI:174871
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Best Local Similarity 86.39
Matches 88; Conservative
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                                                                                            Alu repeat.
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ORGANISM
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                                  DEFINITION
                                                    ACCESSION
VERSION
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HUMALCE221
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AUTHORS
TITLE
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               /organism="Homo sapiens"
/db_xxef="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Direct Submission
Submitsed (12-400-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12730 GTAGAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 12789
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Shaikh,T.H., Roy,A.M., Kim,J., Batzer,M.A. and Deininger,P.L.
cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Pred. No. 0.0058;
0; Mismatches 16;
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Pred. No. 0.0054;
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Human small cytoplasmic Alu transcript.
U67804
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/db_xref="taxon:9606"
/clone="TscAlu3"
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Best Local Similarity 85.0%;
Matches 91; Conservative
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Best Local Similarity 90.6'
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Homor sapiens

Homor sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 108)

Horsthemke, B., Belisiegel, U., Dunning, A., Havinga, J.R.,

Williamson, R. and Humphries, S.

Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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1 (bases 1 to 110)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
Location/Qualifiers
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6 CCTGTAATCCCAGCTACACGGGAAGCTAAGGCAGGAGAATCGCTTGAACCCGGGAGGCGG 65
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL
density lipoprotein.
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Human carcinoma cell-derived Alu RNA transcript, clone CE43.
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llarity 84.0%; Pred. No. 0.014;
Conservative 0; Mismatches 17; Indels (
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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                                                                            66 AGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Wrera2D1"
/dev_stage="embryo"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="carcinoma" 31 c 34 g 18
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83.7%; Pred. No. 0.027;
ative 0; Mismatches 17;
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/note="intron XII fragment"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Alu repeat"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Human gene signatu Microsatellite seg Human gene signatu	ALIGNMENTS  X12095; standard; DNA; 108 BP. X12095; standard; biallell; human; forensic, paternity testing; disease; detection; hencitylic; human; forensic, paternity testing; disease; antoinmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss. W09820165-A2. W09820165-A2. X100313. W09820165-A2. X100313. W198-12095; us-010045; WHITEHEAD INST BIOMEDICAL RES. WHAL1999; us-010045; WHITEHEAD INST BIOMEDICAL RES. WWHAL1997; used not clot acqueents from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or hencebyle typing for diseases W198-20-X1097; are human DNA fragments which contain biallelic polymorphic antich may be appropriate into polymorphic forms in an individual for use in e.g. forensics, paternity appropriate using the primers represented by the appropriate into polymorphic forms in an individual for use in e.g. forensics, paternity polymorphic syndic forms in an individual for use in e.g. forensics, paternity polymorphic syndic forms in an individual for use in e.g. forensics, paternity and sucception syndic and seases in an adversal action of the properties indicated by the appropriate diseases, inclammation; fangs and characteristics such as agammaglobulinenia, diabetes insipiduae, Leschroky pathogenia microorganisms, and characteristics such as unicolamne, octeogenesis imperfecta, acute intermittent porphypria system, infection by pathogenic microorganisms, and characteristics such as unicolamne, octeogenesis inperfecta, acute intermittent porphypria an also be used to produce medicaments for the treatment or Sequence 108 Bp; 19 A; 23 C; 28 G; 37 T;  ry Match  r
993 93 110 667 68	ALIGNMENT  ALIGNMENT  The fragment  The farmation
T24093 T24893 T2048031 T203128 T26410 T24667 T23942 T23942	P. DNA for any fetchar inflament for any fetchar information and for any fetchar in any
анананана	108 BP  rtry)  rtry)  rtyping  rec;  BIOME  ang D;  BIOME  rec form  rec for
81 62 65 99 99 91 101 105 82	ALIGNMA  X12095 standard; DNA; 108 BP.  X12095;  30-MAR-1999 (first entry) Humnn biallelic polymorphic DNA fragmetection; phenotypic typing; charact autoimmune disease; cancer; inflammat. treatment; marker; ss.  WOSS 20165-A2.  WOY-1999; US-030455.  GE-NOV-1997; US-0313.  WARTIFERAD INST BIOMEDICAL RES Hudson T, Lander ES, Wang D;  WPI : 80-286974/25.  GE-NOV-1997; US-0313.  GE-NOV-1997; US-0313.  GE-NOV-1997; US-0313.  GE-NOV-1997; US-0313.  GE-NOV-1997; US-0313.  WOR isolated nucleic acid segments fragments markers which have been isolated usin x80121-X10268. The base occupying the the appropriate IUPAC-IUB ambiguity of methods for determining polymorphic fersions of determining polymorphic fersions and alabetes muscential ty testing or such as agammasjobulinemia, diabetes musch of chermining polymorphic fersions of such diseases, inflammation, casystem infection by pathogenic microasystem inferapeutic treatments. The segments can also be used to produce in the prophylaxis of such diseases.  Esegments can also be used to produce for the Local Similarity B2.68; Pred. NO ches 76; Conservative 1; Misma ches
	((first lic pol) DN ((first lic pol) DN ((first lic pol)) ((first
00000000000	standard; D standard; D sullelic po hism; biallelic po hism; biallelic po hism; benoty liens. 55-A2. 1997; U2031 1098; U2031 1
	nd and a second an
8 8 8 8 6 7 7 8 8 8 9 8 9 8 9 9 9 9 9 9 9 9 9 9 9	5. standard; 15. R-1999 (fir. R-1999) (fir. bhallelic policition; phenot; marker sapiens. Sapiens. V-1997; U203 W-1997; U203 W-1998; U2
8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	X12095 standard; DNA; X12095, standard; DNA; X12095, an Human biallelic polymorphism; biallelic biallelic biallelic autoinmune disease; catreatment; marker; ss. HOMO sapiens. WO9820165-A2.  14-MAY-1998.  05-NOV-1996; US-030455 (WHED ) WHITEHEAD INSTHUGEN T, Lander ES, WWI; 98-28674/25.  New isolated nucleic adetermining polymorphic string or phenotypic Claim 1; Page 219; 310.  X10269-X12937 are huma markers which have been x09121-X10268. The bast the appropriate IUPACmethods for determining such as agammaglobulin muscular dystropph; Wihypercholesterolemia, spherocytosis, von Wilhamorrhad, ctelangleesyndrome, osteogeneals autoimmune diseases, is system; infection by Fas Inneapeutic t segments can also be u prophylaxis of such diseaset Local Similarity Best Local Similarity Best Local Similarity Best Local Significants
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Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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              Human gene signature HUMGS06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
HOMO Sapiens.
W09514772-A1.
01-JUN-10-0-
                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that
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Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

W09514772-A1.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MAISUBARA K.
(OKUB/) OKUBO K.
MAISUBARA K. OKUBO K;
WPI; 95-206931/27.
                                                                                                                                                                                                                                                       01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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(OKUB/) OKUBO K.
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A single-stranded DNA, which complementary strand or the corresp.

A single-stranded DNA, which comprises one of the 7837 "GS" sequences glube in 171001-1726837 and which is able to hybridise to part of human genomic DNA, cDNA or mNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 18 A; 33 C; 28 T;
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double-stranded DNA, which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-coriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (sep. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ATCTCCTGACCTCGTCATCCGCCCGINTCGGCCTCCCATAGTGCTGGGNTTACAGGCCATG 61
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Human gene signature HUMGS07131.
Human gene signature: messenger RNA: mRNA; relative abundance; frequency;
human; cloning; mespeng; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
WO9514772-A1.
for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                               Claim 1; Page 2182; 2245pp; Japanese.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504
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WPI; 95-206931/27.
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frequency;

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Claim 1; Page 1944; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

A single-stranded DNA) which comprises one of the 7837 "65s sequences

Gouble-stranded DNA) which comprises one of the 7837 "65s sequences

Given in T19001-T256837 and which is able to hybridise to part of

human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

untranslated sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance Irequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 TGAGACAGNNTCTCACGCTGTCACCNAGGCTGGAGCGCAGGAGTGCCATCTCAGCTCACT 31
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Human gene signature HUMGS06998.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
                                          Human gene signature HUM5, RNA. Gene signature imassenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 0.98;
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Sequence 91 BP; 18 A; 22 C;
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                      (first entry)
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Best Local Similarity 79.89
Matches 71; Conservative
                                                                                                                                                                                         01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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WPI; 95-206931/27.
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                                                                                                                                              Homo sapiens.
WO9514772-Ai.
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                           2-0CT-1996
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                                                                                                                                                                  285 ITTGTTTGTTTTTTTGAGATAGAGTCTTCCTCTGTCATTCAGGCTGGAGTGCAGTGG 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. Homo saplens.
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                                                                        Length 108
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                                                                                                                                                                                                                                                                  345 CATGATCTCAGCTCACTGCAGCCTCCGCCTCCCGGGTTCAAGAGAT 390
                                                                                                                                                                                                                                                                                             DB 1;
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                                                                   Score 64; DB 1;
Pred. No. 0.64;
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  56
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31
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Human gene signature HUMGS07131.
                                                                   Query Match 0.3%;
Best Local Similarity 74.5%;
Matches 79; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 73.8
Matches 79; Conservative
34
  BP:
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WPI; 95-206931/27.
108
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  Sequence
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RESULT T25009

T25854 standard; cDNA to mRNA; 91 BP

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õ 음 RESULT T25854/c ID T2589

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Gaps

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Length 91; 18; Indels

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28 G;

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Query Match
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T26728
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                         double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-125837 and which is able to hybridise to part of part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) command genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) command genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) command genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) is comparable from the signature of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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WPI; 95-206311/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
WO9514772-A1.
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Pred. No. 1.7;
0; Mismatches 25; Indels
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Claim 1; Page 1720; 2245pp; Japanese.
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Best Local Similarity 74.7%;
Matches 74; Conservative (
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which ts able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using pridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 97 BP; 19 A; 27 C; 20 G; 28 T;
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                                                                                                                   7311 ATCGCTTGAACCCAGGAGGTGGAGGTTGCATTGAGCCAAGATCATGCCACTGCACTCCAG 7370
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Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 2.5;
0; Mismatches 16; Indels
   DB 1; Length 103;
                                                            Indels
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                                                         25;
                                                      0; Mismatches
   Score 60;
                                 Pred. No.
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ID T26213 standard; cDNA to mRNA; 103 BP.
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0.2%;
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                                                         75; Conservative
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01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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Best Local Similarity 81.0
Matches 68; Conservative
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                              Similarity
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                                 Best Local
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A single-stranded DNA (or its complementary strand or the corresp.
Cdouble-stranded DNA) which comprises one of the 7837, "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
chuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
c from various human tissues; synthesis of cDNA wis intitated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
cuntranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
CC sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
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Gene signature: messenger RNA: mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                              e.9
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A single-stranded DNA (or its complementary strand or the corresp.
double-stranded DNA) which comprises one of the 7837 "GS" sequences
r RNA; mRNA; relative abundance; frequency non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 58.4; DB 1; Length 103; 74.0%; Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CATAGCTCACTGTAACACCAAACTCCTGGACTCAAGTGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                 cell typing; abnormal cell function; ss.
Gene signature; messenger RNA; mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T20927 standard; cDNA to mRNA; 103
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                                                                                                                   01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATES/) MATEGBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 74.0
Matches 74; Conservative
                          human; cloning; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                       Okubo K;
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                                                                                                                                                                                                                                                                              WPI; 95-206931/27
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                                                                              saptens.
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Claim 1; F
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Claim 1: Page 623; 2245pp; Japanese.

Claim 1: Page 623; 2245pp; Japanese.

Claim 1: Page 623; 2245pp; Japanese.

Claim 2: Claim 3: Claim 
c given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by in the particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 27 G; 21 G; 31 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20601 GATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGACGTGTGTCACCACACACTGG 20660
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Pred. No. 6.5;
0; Mismatches 26;
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Sequence 107 BP; 26 A; 29
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Best Local Similarity 72.6
Matches 69; Conservative
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Matches 73; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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(OKUB/) OKUBO K.
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WPI; 95-206931/27
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X12085;
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            7084 ATTCCAAAGCTTCTTTTAGAAATAATATTGCTGGGCCAGGCATGGTGGCTCATGCCTGTA 7143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.20-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment EST98276a.

Folymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typhing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                            Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
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                                                                7144 ATTCCAGCACTTTGGGAGGCCGAGGCAGGCAGATC 7178
                                                                                35 ATTCCAGNACTTTGGGAGGCTTAGGTGCGCGGATC 1
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Claim 1; Page 2182; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 C;
                                                                                                                                                            T26828 standard; cDNA to mRNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recognising different cell types
Sequence 108 BP; 18 A; 3
                                                                                                                                                                                                     Human gene signature HUMGS09078.
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                                                                                                                                                                                    14-NOV-1996 (first entry)
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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                                                                                                                                                                                                                                                                                                                                                       Okubo K;
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Best Local Similarity
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WO9514772-A1.
01-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                        Matsubara K,
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16-NOV-1997, U20313.

16-NOV-1996; UG-30455.

16-NOV-1996; UG-30455.

16-NOV-1996; UG-30455.

18-MED ) WHITEREAD INST BLOMEDICAL RES.

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Polymorphism: biallelic; human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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Best Local Similarity 72.9
Matches 70; Conservative
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the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch Nyhan syndrome, can the construction of the construction 
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ó 0; Gaps Score 55.6; DB 1; Length 100; Pred. No. 8.4; 1; Mismatches 25; Indels Query Match 0.2%; Best Local Similarity 72.9%; Matches 70; Conservative 1 õ g

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Search completed: June 21, 2000, 07:57:11 Job time: 586742 sec

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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Contact: Wilson RK
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AQ004934 CIT-HSP-2
N25299 yw52c09.s1
AA381369 EST94442
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AQ062963 CIT-HSP-2
H11143 ym09c06.rl
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AQ535244 RPCI-11-3
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AA385808 EST99495
B17434 345K2.TVB C
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashUrWI human EST Project
Unpublished (1997)
on Sep 12, 1996 this sequence version replaced gi:1397630.
Description
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AA565533
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                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@mage.llnl.gov) for further information.
Seq primer: -26ml3 rev1 ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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High quality sequence stop: 102.
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94.3%; Pred. No. 0.14
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA243009
AA243009.1 GI:1873869
                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 100; Conservative
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Fax: 314 286 1810
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1. .108
/organism="Homo sapiens'
/db_xref="GDB:7043860"
/db_xref="taxon:9606"
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/clone_llb="CIT-HSP"
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                                                                                                                                                                                                                                                  / Match 0.4%;
Local Similarity 94.1%;
nes 96; Conservative
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B65160.1 GI:2639138
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ORIGIN
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SOURCE
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B65160
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                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

S 1 (bases 1 to 103)

NOT-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

L Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151346.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 4961150

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA807640 103 bp mRNA EST 05-WAR-1998 nx08b05.sl NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255473 3' similar to contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12724 TITITAGIAGAGACGGGTITCACCAIGITAGCCAGGAIGGICTCGAICTCCTGACCTCG 12783
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TITITAGTAGAGGGGTTTCACCGTGTTAGCCAGGATGGTCTTGATCTCCCTACCTCG 63
                                                                                                                                                                                                                                                                                                                                                                              Query Match

0.4%; Score 94.8; DB 30; Length 109;
Best Local Similarity 93.4%; Pred. No. 0.2;
Matches 99; Conservative 0; Mismatches 7; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism=_nosmonsorpress
/db_xref="taxon:9606"
/clone="IMAGE:1255473"
/clone_lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
                                   /organism="Homo sapiens"
/db_xref="GDB:5426481"
/db_xref="taxon:9606"
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 Location/Qualifiers
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AA807640.1 GI:2877108
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DEFINITION
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AUTHORS
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FEATURES
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Constructed by Bento Soares and M. Fatima Bonaldo."

Total Library 1st strand cDNA was prepared from 3 pooled polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was 11gated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

27 c 30 g 27 t
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Other GSSs: CIT-HSP-2017G2.TFB
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Clones are available from Research Genetics (Info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 12729 AGTAGAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC 12788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a random BAC End Sequence Database for Sequence-Ready Map Bullding
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Adams.M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
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CIT-HSP-2017G2.TRB CIT-HSP Homo sapiens genomic clone 2017G2,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92.4; DB 38; Length 103;
Pred. No. 0.38;
0; Mismatches 6; Indels 0
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Matches

g ŏ g DEFINITION

AA897366

RESULT

ACCESSION

VERSION KEYWORDS

AUTHORS

JOURNAL

COMMENT

FEATURES

REFERENCE

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EMEATORIES Manumalia; Bukaryota; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metrazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

EL (bases 1 to 109)

Adams, M. D., Rounsley, S. D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           974. 1701: 301 838 0200
Fax: 301 838 0208
Fax: 302 838 0208
Fax: 303 838 0208
Fax: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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                                                                                                                                                     AQ028426 109 bp DNA GSS 30-JUN-1998 CIT-HSP-2313G15,TF CIT-HSP Homo sapiens genomic clone 2313G15, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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   61 CTCATGATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATTATAGGCGTG 110
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Pred. No. 0.47;
0; Mismatches 11;
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/db_xref="taxon:9606"
/clone="2313G15"
/clone_lib="CIT-HSP"
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GSS.
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nes 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Endi: (301) 496-1550
Endi: (301) 496-1550
Endi: Robert Strausberg(hih.gov
This clone is available rogalty-free through LLNL; contact the IMAGE Consortium (Info@image.llnl.gov) for further information. Insert Length: 834 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 63.
Location/Qualifiers
                                                                                                                                              7261 TGGTGGCAGGCACCTGTAATCCCAGCTATTCAGGAGGCTGAGACAGGAGAATCGCTTGAA 7320
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Pred. No. 0.37;
0; Mismatches 11; Indels 0
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       Length 108;
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                                                                            Indels
                                                                                                                                                                                                                                                                                                                             61 CCCGGGAGGTGGAGGTTGCAGTGAGCCAAGATCATACCACTGCACAC 107
Score 92.6; DB 84;
Pred. No. 0.35;
0; Mismatches 9;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1466067"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                       Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                             end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                   Use of a random BAC End Sequence Database for Sequence-Ready Map
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jan 24, 1995 this sequence version replaced gi:634306.
Context: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 0.4%; Score 91; DB 84; Length 108; 1 Similarity 90.7%; Pred. No. 0.52; 97; Conservative 0; Mismatches 10; Indels
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                                                                                                                                                               Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="GDB:7043860"
/db_xref="taxon:9606"
/clone="2017G2"
                                                                                                                         Unpublished (1997)
Other_GSSs: CIT-HSP-2017G2.TFB
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ak64h01.sl Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412689 3' similar to contains Alu repetitive
element;contains element KER repetitive element ;, mRNA sequence.
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1 (bases 1 to 101)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
On Nov 29, 1993 this sequence version replaced g1:636191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20507 TTTTTTTTTTGAGATGGAGTCTTGCTTTGCTGCCCAGGCTGGAGTGCAGTGCCATGATCTC 20566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortlum (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY 20567 GGCTCACAGCAACCTCCACCTCCTGGGTTCAAGTGATTCTCCTGCCTCA 20615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGAGATTCTTCTGCCTCA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 30;
                                                                                                                                                    Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 90.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constructed by David Krizman."
26 c 28 g 38 t
                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 90.4; Di
Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1007406"
/clone_lib="NCI_CGAP_Prl"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA835205.1 GI:2908933
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FEATURES

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SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.G.

Uppublished (1997)

Londact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: maddams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
                                                                                              /note="vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1; CalTech Human BAC Library D"
1 30 c 34 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                                                                          12739 GGGTTTCACCATGTTAGCCAGGATGTCTCGATCTCCTGACCTCGTGATCCGCCCACCTG 12798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
28 c 30 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B48914 103 bp DNA GSS 08-APR-1999 RPCI11-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GGGTTTCACCATGTTAGCCAGGACGTCTTGATCTCCTGACCTCGTGATCCACCCGCCTC 47
                                                                                                                                                                                                                                                                                                         Length 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                     0.4%; Score 88.4; DB 105;
ilarity 89.6%; Pred. No. 0.99;
Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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/cell_type="Lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Homo sapiens"
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/db_xref="taxon:9606"
/clone="RPCI-11-4A12"
/clone_lib="RPCI-11"
/clone_lib-"CITBI-E1"
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1..103
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                                  /sex="male"
/cell_type="sperm"
/note="Vector: pBel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
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B48914.1 GI:2601151
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Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends
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Best Local Simi
Matches 95;
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SOURCE
ORGANISM
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ORIGIN
                                                                                                                                                                    BASE COUNT
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JOURNAL
COMMENT
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LOCUS
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                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                  /dev_stage="adult, 34 years"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
lit strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3'); double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
36 c 27 g 24 t
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Ontbulished (1998)
Ontbulished (1998)
Cottact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Company Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo saplens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M3-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14076 TGAGACGGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACT 14135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGAGACGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGCTTGATCTCGGCTCACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ264176 106 bp DNA GSS 27-OCT-1998 CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2, genomic survey sequence.
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                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:1412689"
/clone_lib="barstead pancreas HPLRB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O.4%; Score 89.8; DB 39;
Similarity 93.1%; Pred. No. 0.72;
44; Conservative O; Mismatches 7;
ET from Amersham.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2509A2"
                                                                                              /organism="Homo sapiens"
                           Location/Qualifiers
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-40m13 fwd.
                                                                                                                                                                                                                                   /sex="female"
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AQ264176.1 GI:3792743
   Sed primer:
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SOURCE

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

VERSION KEYWORDS ACCESSION

LOCUS AQ264176/c

Query Match Best Local (

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Homo sapiens
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                               AA228795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
NAI-Onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   TTTTTAGTAGAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCG 12783
                                                                                                                                                                                                                                                                                                                                                               3
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                                                                                                                                                                                                                                                                                                                               AA565533 107 bp mRNA EST 08-SEP-1997 nk42b11.s1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1016157 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                            40
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Pred. No. 1.1;
0; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 14165 TCTCCTGCCTCAGACTCCCGAGTAGCTGGGATTACAGTCATGCACCA 14211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 1661 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ww-bio.llni.gov/bbrp/image/image.html
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/db_xref="taxon:9606"
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AA565533.1 GI:2337172
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Matches 95; Conservative
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ORIGIN
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TITLE
12724
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KEYWORDS
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                                                                                                                                                                                                                                                                                                      AA565533
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Tunor Gene Index On the Institute, Caner Scione Figure (Corr), Tunor Gene Index (1997)

On Sep 12, 1996 this sequence version replaced gi:1394473.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //note="Vector: pawpl0; Site_1: Not1; Site_2: EcoR; ist strand cDNA was primed with ollgo(dT)17 on 50 ng of DNAsce-treated, total cellular RNA obstained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor specific primer, and the resulting PCR product subcloned into pAMPIO by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
AA228795 103 bp mRNA EST 20-AUG-1997 1014607.31 NCI_CARP_PTI Homo sapiens CDNA clone IMAGE:1008132 similar to contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 103) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3786 TITITITITITITICAGACGGTGTCTCACTCTTCCGCCCAGGCCGGACTGCAGTAGCGCTAT 3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnj.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="texon:9606"
/clone="IMAGE:1008132"
/clone_11b="NCI_CGAP_Pr1"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 81.
Location/Qualifiers
                                                                                                                                                                         AA228795.1 GI:1851455
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AQ582186

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Search completed: June 21, 2000, 01:05:59 Job time: 563326 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library availability, please contact Pieter de Jong (pleterédejong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq primer: SP6
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                                                                                                                                                                                                                                Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Yenter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20061 GGAGTGCAGTGCACAATCTCGGCTCACTGCAACCTCCGCCTCCGGGTTCAAGCTATTC 20120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hbe@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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  07-JUN-1999
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
                                                                                                                                                                                                                                                                                                               Unpublished (1997)
On Feb 19, 1999 this sequence version replaced g1:4146076.
On Feb 19, 1999 this sequence version replaced g1:4146076.
On Feb 19, 1999 this sequence version replaced g1:4146076.
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fex: 301 838 0200
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0
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AQ582186 103 bp DNA, GSS 07-
RPCI-11-451A15.TJ RPCI-11 Homo sapiens genomic clone
RPCI-11-451A15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86.8; DB 108;
Pred. No. 1.5;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QY 20121 TCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGC 20159
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/db_xref="GDB:7672814"
/db_xref="taxon:9606"
/clone="RPCI-11-451A15"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .103
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AQ584425.1 GI:5011535
                                                                                   AQ582186.1 GI:5009296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 0.4%;
1 Similarity 91.9%;
91; Conservative (
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Best Local
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AQ584425/c
LOCUS
DEFINITION
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ORGANISM
LOCUS
DEFINITION
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                                                                                                                                              ORGANISM
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                                                             ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                    AUTHORS
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                                                                                                     KEYWORDS
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                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                         COMMENT
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
                          Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Venter BAC.
Use of BAC.
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12737 CGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCACC 12796
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                                                                                                                      Unpublished (1997)
Other GSSs: RPCI-11-458L2.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
1911: 301 838 0208
Pax: 301 838 0208
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/note="Vector: pBACe3.6;
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/clone="RPCI-11-458L2"
/clone_lib="RPCI-11"
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  1 (bases 1 to 103)
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Best Local Similarity
Matches 93; Conserv
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REFERENCE
                             AUTHORS
                                                                                                                              JOURNAL
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Pc-DoS/Ms-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFTCATION A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.2; DB 4;
Pred. No. 4.9e-06;
US-08-454-557C-69
US-08-340-426D-69
US-08-450-673C-69
US-08-450-657
US-08-454-557C-60
US-08-340-426D-57
US-08-340-426D-60
US-08-340-426D-60
US-08-340-426D-60
PCT-US95-17111A-57
PCT-US95-17111A-57
US-08-450-673C-60
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APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Pro
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/08481658B
; Patent No. 5955075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: 30,863
REPERENCE/DOCKET NUMBER: D-OC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-2077
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
     COMPUTER READABLE FORM:
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Best Local Similarity
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US-08-481-658B-65
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US-08-481-658B-65
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 STATE:
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10039.516 Million cell updates/sec
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                                                                                                                                                                                                            Sequence 65,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-477-504A-65
US-08-485-756A-65
US-08-485-8565
US-08-787-733-65
US-08-454-557C-91
US-08-450-673C-91
US-08-450-673C-91
US-08-450-673C-91
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US-08-450-673C-91
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US-08-454-557C-70
US-08-340-426D-70
US-08-450-673C-70
PCT US95-17111A-70
US-08-440-426D-92
US-08-340-426D-92
US-08-340-426D-92
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US-08-486-756A-65
US-08-485-862B-65
US-08-787-739-65
US-08-332-766A-36
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US-08-481-658B-65
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 110
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Perfect score:
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US-08-486-756A-65
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  0; Mismatches 18; Indels
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                                                                                                                                                    61 CTGACCTTGTGATCCACCCTCGGCCTCCCAAGTGCTGGGAT 105
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Pred. No. 4.9e-06;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION MADA:
APPLICATION MABER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 0.0021,3D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         0S-08-477-504A-65; Sequence 65, Application US/08477504A; Patent No. 5972353; Betent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 82.9
Matches 87; Conservative
87; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
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US-08-477-504A-65
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,756A

FILING DATE: 07-JUN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTONNEY, AGBNT INDRMATION:

NAME: LAUGHER, LOORA L.

REGISTRATION NUMBER: 30,863

REGISTRATION NUMBER: D-0021.3C

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-435-2034

TELEPHONE: 415-435-0727

SEQUENCE CHARACTERISTICS:
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Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 MATIPOSA COURT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 65, Application US/08485862B
Patent No. 5989838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                    CITY: Tiburon
                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                  ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-486-756A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-485-862B-65
                                                                                                                                                                                                                                                                                                               COUNTRY:
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FILING DATE: 24-7AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.3%;
82.9%;
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.99
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ZIP: 20005-3934
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY 12715 TTTTGTATTTTTAGTAGAGGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 12774
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                                                                                                                                                                                                                              SOFTWARE: Petantin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT: IRFORMATION:
NAME: Lauder, Leona L.
REGIERRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OY 12775 CTGACCTCGTGATCCGCCCACCTGAGCCTCCCAAAGTGCTGGGAT 12819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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Fatent No. 6027887
GENERAL INFORMATION:
APPLICANT: Pastorekova, Silvia
APPLICANT: Pasto
                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
             California
                                                USA
                                                                         94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-485-862B-65
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                                         COUNTRY:
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RESULT 0
18-08-454-557C-91
5 Sequence 91, Application US/084555C
7 Patent No. 5830670
6 GENERAL INFORMATION:
7 APPLICANT: de la Monte, Suzanne
7 APPLICANT: Mands, Jack R.
7 TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
7 TITLE OF INVENTION: of Alzheimer's Disease
7 TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                      12715 TTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 12774
                                                      Gaps
                                                                                                                                ó
Score 76.2; DB 5; Length 105;
Pred. No. 4.9e-06;
0; Mismatches 18; Indels
                                                                                                                                                                                                    Qy 12775 CTGACCTCGTGATCCGCCCACCTGAGCCTCCCAAAGTGCTGGGAT 12819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SECURICES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                   61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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TYPE: nucleic acid
                                                      both
                               STRANDEDNESS:
; TOPOLOGY: bot
US-08-340-426D-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-450-673C-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: Of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12747 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCACCTGAGCCTCCC 12806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 3; Length 84;
Pred. No. 0.00023;
0; Mismatches 10; Indels
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COMPUTRY: U.S.A.
21P: 2006-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
FELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: Ludday, Steven R.
REGISTRATION NUMBER: 0609.3840003
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHON: (202) 371-260
TELEPHON: (202) 371-240
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: MODELOGY both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 91, Application US/08340426D Patent No. 5948634 GENERAL INFORMATION: APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY 12807 AAAGTGCTGGGATTACAGGTGTG 12829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAAGTGCTGGGATTACAAGCGTG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%;
Best Local Similarity 88.0%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-454-557C-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-08-340-426D-91
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GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QY 12747 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCACCTGAGCCTCCC 12806
                                                                                               QY 12747 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCACCTGAGCCTCCC 12806
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Pred. No. 0.00023;
0; Mismatches 10; Indels
  Length 84;
                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: FILIPOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-LEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/POCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
  Score 67; DB 4;
Pred. No. 0.00023;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 91, Application US/08450673C; Patent No. 5948888
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                                                                                                                                                                                               Qy 12807 AAAGTGCTGGGATTACAGGTGTG 12829
                                                                                                                                                                                                                             61 AAAGTGCTGGGATTACAAGCGTG 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.3%;
Best Local Similarity 88.0%;
Matches 73; Conservative (
  0.3%;
Query Match 0.39
Best Local Similarity 88.09
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-3934
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US-08-454-557C-91
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US-08-454-557C-91/c
Sequence 91, Application US/08454557C
Sequence 91, Application US/08454557C
Sequence 91, Application US/08454557C
SENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
UNMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12747 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCACCTGAGCCTCCC 12806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                               APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                           ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 Washington STATE: Dath.
                                                                                                                                                                                                                                                                 SIATE: D.C.
COUNTRY: U.S.A.
ZIP: Z0005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Elloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGRIT IRFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 67; DB 6; B8.0%; Pred. No. 0.00023; Ative 0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0609.3840002
PCT-0595-17111A-91; Sequence 91, Application PC/TUS9517111A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 12807 AAAGTGCTGGGATTACAGGTGTG 12829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-260
TELEPRA: (202) 371-260
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
PCT-US95-17111A-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAAGTGCTGGGATTACAAGCGTG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.3%
Best Local Similarity 88.0%
Matches 73; Conservative
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TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTONREY/AGERT INFORMATION:
NAME: LIGHING, Steven R:
REGISTRATION NUMBER: 36,203
REFERENCE/POCKET NUMBER: 36,203
REFERENCE/COCKET NUMBER: 36,203
RECEDEMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEFRAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91: SEQUENCE CHRARATESTICS:
LENTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATURNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-34-0426D-91/c
S-08-34-0426D-91/c
Sequence 91, Application US/08340426D
Patent No. 5948634
GENERAL INFORMATION:
APPLICANT: Gala Monte, Suzanne
APPLICANT: Gands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7194 CAAGACCAGCCTGACCAATATGG 7216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     both
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23 CGACACCAGCCTGATGAACATGG
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US-08-454-557C-70
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PERERAL INFORMATION:

APPLICANT de la Monte, Suzanne
APPLICANT WANGS, Jack R.

TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS: 121
CORRESPONDENCE ADDRESS: Assler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM PC COMPATION
COMPUTER: STATES: 30-MAX-1995
COMPUTER: STATES STATES: 30-MAX-1995
CLASSIFCATION: MUMBER: 35,203
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-250
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                    Score 60.6; DB 4; Length 84;
Pred. No. 0.0036;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 60.6; DB 4; Length 84; 13.1%; Pred. No. 0.0036; ve 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 91, Application US/08450673C
; Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                       7194 CAAGACCAGCCTGACCAATATGG 7216
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                                                                                                                                                                                      Query Match 0.2%;
Best Local Similarity 83.1%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 83.1%;
Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 84 base pairs
nucleic acid
EDNESS: both
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Best Local Similarity
Matches 69; Conserv
                                                                                                     ; TOPOLOGY: both US-08-340-426D-91
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US-08-450-673C-91/c
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Matches
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Patent No. 5830670
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                           APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 84;
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                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60.6; DB 6;
Pred. No. 0.0036;
0; Mismatches 14;
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CLASSIFICATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTOREY/ABENT INFORMATION:
NAME: Ludwig Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STATES
INFORMATION FOR SEQ ID NO: 91:
SEGURENCE CHARRACTERISTICS:
LENGTH: 84 base pairs
TTYPE: NUMBER: No. 1
PCT-US95-17111A-91/c; Sequence 91, Application PC/TUS9517111A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7194 CAAGACCAGCCTGACCAATATGG 7216
                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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Best Local Similarity 83.19
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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Search completed: June 21, 2000, 05:22:58
Job time: 577708 sec
TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                     Query Match 0.29
Best Local Similarity 84.69
Matches 66; Conservative
                                                                                                                                                                                                   ; TOPOLOGY: both US-08-340-426D-70
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Sequence 70, Application US/08340426D
Sequence 70, Application US/08340426D
Patent No. 5946634
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY 16969 ACCACGCCTGGCTAATTTTGTATTTCTGGTAGACGGGGTTTCACCATGTTGGCCAGG 17028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATONREY AGENT INFORMATION:
                                                                                            ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
                                                                                                                                                                                                                                                                  CLASSIFICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2500
LINFORMATION FOR SEQ ID NO: 70: SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                    0609.3840003
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                          Washington
                                                                         RY: U.S.A.
20005-3934
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                       CITY: Wa:
STATE: D
COUNTRY:
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                                                                                                                                                                                                                              0.2%; Score 58.8; DB 4; Length 78; 84.6%; Pred. No. 0.0075; tive 0; Mismatches 12; Indels
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANBENESS: both
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gb_htg10:*
gb_htg11:*
gb_htg12:*
gb_htg13:*
gb_htg14:*
       em_htg1:*
em_htg2:*
em_htg3:*
em_hum5:*
                                      gb_pl3:*
gb_pr5:*
gb_htg8:*
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64.4
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                                                  June 14, 2000, 12:38:36; Search time 17971.8 Seconds (without alignments) -1569.738 Million cell updates/sec
                                                                                   370290
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                          882769 seqs, -486395729 residues
                                                                                                                                                                                                Post-processing: Minimum Match 0%
Listing first 45 summaries
                                     OM nucleic - nucleic search, using sw model
                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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9b_bal:*
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9b_bal:*
9b_pat:*
9b_pat:*
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9b_pl:*
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                                                                                                                                                                        Minimum DB seq length: 10
Maximum DB seq length: 110
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Perfect score:
                                                                                                                   Scoring table:
                                                                                                                                                                                                                         Database :
                                                                                                     Sequence:
                                                                                                                                           Searched:
                                                     Run on:
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46: em\_htg1:\*
47: em\_htg2:\*
48: em\_htg2:\*
49: em\_htg2:\*
50: gb\_pt3:\*
51: gb\_htg8:\*
52: gb\_htg9:\*
53: gb\_htg1:\*
54: gb\_htg10:\*
55: gb\_htg1:\*
55: gb\_htg1:\*
56: gb\_htg1:\*
56: gb\_htg1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ID	TOCAL ANDREAS	HIMALCE162	0 HSLDLRN2	) HSLDLRN2			1 HSU67803	Ξ	1 HSU67804	Ŧ						0 879560	HUMHGAL	X		3 G32614	Ξ				3 HUMUT8002B	HUMLDLRAI	HUMGALNSA	3 HSBICBR	HUMALCEZ/Z	#UMALCE162		Ξ	HUMLDLRA2	3 HUMUT7692A			HUMALCE43	HUMBRKFAE				O HSSTHPKIB	NVIHIS2A	HUMLDLRDJ
Length DB	103 0		·	Н	_	-	-	σ	-	σ	٦.		103 13		Π,	7	₹	0	_	-	σ		٦,	٠,	95 1		100			ν-	٦.	97	97 9	7	1		110 9		7		0	2	96	97 9
Query Match			0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.7	0.5	0.5	0.5	0.5	0.5	0.5		0.5	0.5	0.0	7.0	0.0	7.0	7.0	9 0	0.5	0.5	0.5	0.5	0.3			•		0.5	0.5	0.5	0.5
Score	07.7		87.2	83.6	79.8	79.8	80	75	ഗ	74.2	73.6	73.4	73	73	73	72.4	71.6	70.8	70.8	8.69	8.69	. 1	69	68.8	68.4	Φ,	8.79	89	200	20 2	•	67.2	66.4	65.8	99	99	99	9.59	9.59	65.2	65.4	64.6	64.8	64.4
Result No.		10	3	4	Z.	0 د	c 2	ω		c 10	11	c 12	-	c 14	15	16	17	-	c 19		c 21	22	23	c 24	~	c 26	7	~ ~	200	3.50	7.0	33	m	c 35	c 36	m	38	39	c 40	4	42	43	C 44	c 45

ALIGNMENTS

20-MAY-1992

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

ACCESSION VERSION KEYWORDS

```
1 (bases 1 to 108)
Horsthenke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Williamson, R. and R.
Williamson, R.
Williamson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Biochem. 164 (1), 77-81 (1987)
3564 ITTTTTGAGACGGAGTCTAGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCACCATCTTGGC 3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3618 CTTGGCTCACTGCAAGCTCTGCCTCCCGGGTTTATGCCATTCTCATGTCTCAGCCTCCAG 3677
                                 107 ITITITGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGGATCTCGGC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 crcgcrcacrccacrcrcrccrccrcgcrrcaagcaarrcrccrccrcagccrccc 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alu repetitive sequence; low density lipoprotein receptor.
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                                                                                                                                                                                                                                                                                                                                                                                  Human LDL-receptor gene intron 14 fragment (normal gene).
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Human LDL-receptor gene intron 14 fragment (normal gene)
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                          3624 TCACTGCAAGCTCTGCCTCCCGGGTTTATGCCATTCTCATGTC 3666
                                                                                                                                                              TCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTTCTGCC 5
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Pred. No. 9.1e-06;
0; Mismatches 13;
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23 c 39 g 18 t
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/db_xref="taxon:9606"
1. .108
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Matches 95; Conservative
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HSLDLRN2/C
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ORIGIN
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VERSION
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MEDLINE
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SOURCE
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HSLDLRN2
LOCUS
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1 (bases 1 to 107)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

21 (bases 1 to 103)

21 (bases 1 to 103)

All Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcripts in human embryonal carcinoma cells. J. Mol. Biol. (1992) In press
J. Mol. Biol. (1992) In press
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
                                                        HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
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                                                                                                                                                                                                                       Homo sapiens male embryo carcinoma cDNA to other RNA Homo sapiens
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Homo sapiens male embryo carcinoma cDNA to other RNA
Homo sapiens
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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27 c 33 g 1
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30 c 35 g 1
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/sex="male"
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                                                                                                                                                    M87896.1 GI:174874
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HUMALCE162/C
                          HUMALCE221/c
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ORIGIN
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Matches

ò a ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE

JOURNAL FEATURES

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Gaps

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Indels

Length 108;

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COMMENT

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*Source: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNN.
Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
Millamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
BUT J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. 108
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Shakkh, T.H., Klm,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
                                                                                       HSLDLRD2 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor mutated gene with intron 14 deletion junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3619 TTGGCTCACTGCAAGCTCTGCCTCCCGGGTTTATGCCATTCTCATGTCTCAAGCCTCCAGA 3678
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shaikh,T.H., Roy,A.M., Kim,J., Batzer,M.A. and Deininger,P.L.
CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                            Alu repetitive sequence; low density lipoprotein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
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Human small cytoplasmic Alu transcript.
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1 Similarity 84.1%;
90; Conservative
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U67803.1 GI:2289917
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Best Local Similarity
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SOURCE
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HSU67803/c
                                                                                                         DEFINITION
ACCESSION
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1 (Bases 1 to 108)

1 (Bases 1 to 108)

1 (Bases 1 to 108)

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia for Eur. 3. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See X05248 for corresponding normal gene sequence. In the defective LDL-receptor gene the deletion ocurred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3619 TIGGCICACIGCAAGCICTGCCTCCCGGGITIAIGCCATICICAIGICICAGCCICCAGA 3678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"deletion junction region intron 12/ intron 15" 40~{
m c} 20 g 28 t
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                                                                                                                                                                                                                                                                                                                                                                          3 AAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCGGGAGGTGAGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alu repetitive sequence; low density lipoprotein receptor
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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14.1%; Pred. No. 0.00018;
.ve 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                 DB 10;
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Pred. No. 3.8e-05;
0; Mismatches 14
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23 c 39 g 18 t
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/db_xref="taxon:9606"
                                                                1. .108
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 86.8%;
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Best Local Similarity 84.1
Matches 90; Conservative
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1 (bases 1 to 103)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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89.6%; Pred. No. 0.00016;
tive 0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                       LOCUS HSU67804 108 bp RNA
DEFINITION Human small cytoplasmic Alu transcript.
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                                       1. .108
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
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27 c 33 g 1
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/cell_line="NTera2D1"
/dev_stage="embryo"
                                                                                                                                 /rpt_family="Alu"
/rpt_type=dispersed
39 c 30 g
                                                                                                                    /note="scAlu"
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Best Local Similarity 84.81
Matches 84; Conservative
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Matches 86; Conservative
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Matoba.R., Okubo.K., Hori,N., Fukushima.A. and Matsubara.K.
The addition of 5'-coding information to a 3'-directed cDNA library
improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
94357437
Submitted (21-Jul-1993) to DDBJ by:
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Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo
Matoba, Osaka University, Institute for Molecular and Cellular Bio;
1-3, Yamada-oka, Suita, Osaka 565, Japan
(E-mall:matoba@inherit.imcb.osaka-u.ac.jp,
17-1:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
2 (bases 1 to 108)
                                                                                                                                                                                                                                                       2 (bases 1 to 108)
Shakkh, T.H., Klin, J., Batzer, M.A. and Deininger, P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
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Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scalu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Matoba,R.
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Human HepG2 partial cDNA, clone hmdld03m5.
D16965 GI:598552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.3%; Score 75.2; DB 1
Best Local Similarity 86.5%; Pred. No. 0.0011;
Matches 83; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3795 GCCTGCCTTGGCTTCCCAAAGTGCTGGGATTACACG 3830
                                                                                                                                                                                                     J. Mol. Biol. 271 (2), 222-234 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .108
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type=dispersed
38 c 26 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="TscAlu3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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SOURCE
ORGANISM
                                                                                 RESULT 12
HSU67807/c
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VERSION
                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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MEDLINE
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TITLE
JOURNAL
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KEYWORDS
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1 (bases 1 to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSLDLI12 108 bp DNA PRI 20-MAY-1992 Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY 12226 TTGGCTCACAGCAACCTCCGCCTCCCGGGTTCAAGCCATTCTCCCTGCCTCAGCCTCCGGA 12285
                                                                                                                                                                                                                                                                                                                                        Qy 12222 GATCTTGGCTCACAGCAACCTCCGCCTCCCGGGTTCAAGCCATTCTCCTGCCTCAGCCTC 12281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                         108 GATCTTGGCTCACTGCAACCTCTGCCTCCCGGGNTCAAGCGACTCTCCTGCCTCAGCCTC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TCGCCTCACCACAACCTCTGCCTGCGTTCAAACCATTTCCTGCCTCAGCCTCCTTA 61
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alu repetitive sequence; low density lipoprotein receptor; repetitive sequence.
Research Institute of Innovative Technology for the Earth
                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                      Qy 12282 CGGAGTAGCTGGGATTACAGGCATGCGCCACGACACCCTGGCTAATTT 12330
                                                                                                                                                                                                                                                                          Length 108;
                                                                                                                                                                                                             2 others
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                                                                                                                                                                         Score 74.2; DB 9; Dred. No. 0.0017; 0; Mismatches 15;
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38 c 20 g 29 t
                                                                                                                                                                                                             17
                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
                                                                                                Location/Qualifiers
                                                                                                                                                                                                             38 g
                                 Soraku-gun, Kyoto
Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321.
                                                                                                                                                                                                                                                                         Query Match 0.3%;
Best Local Similarity 85.3%;
Matches 93; Conservative
                  Kizugawadai Kizu-cyo,
                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             density lipoprotein.
X05248
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Matches 85; Conserv
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HSLDLI12
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KEYWORDS
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2864 GTAGAGATGGGGTTTCACTATGTTGGCCAGGCTAGTTTGGAACTCCTGACCTCCAGGTT 2923
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1991
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Primates; Catarrhin1; Homlnidae; Homo.
1 (bases 1 to 103)
Aldridge, F.L.
                                                                                                                                                                                 01-AUG-1997
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Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler, R., Riley, J.H., Ogilvie, D.J., Anand, R., Buxton, J.,
Davies, J., Johnson, R. and Markham, A.F.
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Pred. No. 0.0023;
0; Mismatches 16; Indels
HSBICBR 103 bp DNA STS
Human sequence tagged site BICBR DNA from 19q13.
X57789
                                                                                                                                                                                 PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2924 CCATTCTCATTGGCCTCCCAAAGTGCTGGGATTACAGGC 2962
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Human small cytoplasmic Alu transcript.
U67807
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97415756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
/rpt_type=dispersed
39 c 24 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="scAlu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 0.3%;
Local Similarity 83.8%;
hes 83; Conservative
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
allu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1..108
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Two sequence-tagged sites defining the ends of a 380 kb YAC clone from 19q13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSLDLRD1 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor mutated gene with intron 12 deletion junction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     6399 ATTAGAGATGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGA 6458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"deletion junction region intron 12/ intron 15" 40~{\rm c} 20~{\rm g} t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)
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0
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81.0%; Pred. No. 0.0027;
tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                         Length 103;
                                                                                                                                                                                                                                                                         1 others
                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 13; Length 10
Pred. No. 0.0027;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6459 TCTACCCACCTCAGCCTCCCAAGTGCTGGGATTACAG 6496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 19 (17), 4787 (1991)
91367697
See also X57788 for STS 81C8L.
                                                                                                                                                                                                              /germline
/clone_lib-"YAC library: ICI"
                                                                                                                                                                                                                                                                       ų
                                                                                                                                                                                                                                                                         22
                                                                                                                              1. .103
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19q13"
                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                      /clone="8IC8"
                                                                                                                                                                                                                                                                                                                                                       Query Match 0.3%;
Best Local Similarity 83.7%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X05249
X05249.1 GI:34335
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Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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ORIGIN
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HSLDLRD1/c
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MEDLINE
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AUTHORS
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COMMENT
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*Source: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNN.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                            Eukaryotza, Metazoa, Chordata, Vertebrata, Mammalia, Eutheria, Primates; Catarphini, Hominidae, Homo.

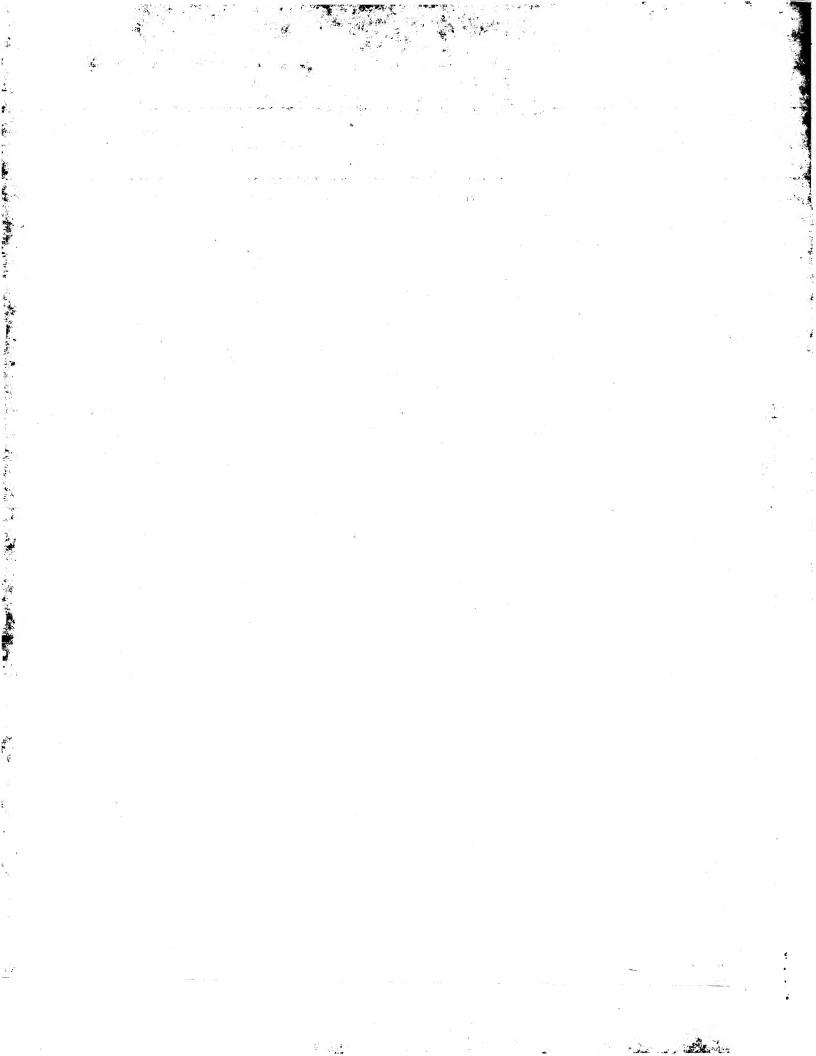
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Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for Eur.

5 Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor mutated gene with intron 14 deletion junction.
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106 AAAAATTAGCCAGGCGTGGTGGTAGGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGC 47
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Alu repetitive sequence; low density lipoprotein receptor
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WPI: 98-286974/25.

Wew isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity

PT determining polymorphic forms for use in e.g. forensics, paternity

PT testing or phenotypic typing for disease

CI aim 1, Page 218: 310pp; English.

X10269-X12397 are human DNA fragments which contain biallelic polymorphic can be used in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in misches for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases cub- as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Andrich syndrome, Fabry's disease, familial typercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary cautoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such can cautoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such can sequents can also be used to produce medicaments for the treatment or more, when a faurch diseases.
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Polymorphism, biallelic; human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament,
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Human biallelic polymorphic DNA fragment EST98276c.
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                         X12085/C
IID 085/C
X1201
DE Human
X1201
X1
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determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
Claim 1; Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insiplidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial phenotytosis, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, hereditary spherocytosis, von Willebrand's disease, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23012 GTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCTGAAGAAGGAGGATCGCTTGAGTC 23071
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Sequences shown in V41230 to V41247 represent nucleotide sequences of sequences shown in V41230 to V41247 represent nucleotide sequences of mouse EST from tagged CDNA clones. These are used in the method of the invention of screening for human developmental genes. The method comprises inserting a promoterless reporter gene into a non-primate mammalian embryonic stem cell (ESC) genome and identifying cellular transcripts that encode the reporter gene product. Fragments of genes encoding these transcripts are cloned and sequenced. A gene encoding the are includes unknown sequences is selected and expression level of the gene encoding the transcript, or part of it, in different cell types and/or different developmental stages is detected. A gene showing differential expression is selected and expression levels of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for human developmental genes - by trapping in murine embryonic stem cells and analysing differential expression in vitro, selecting homologous non-human primate gene and using it to isolate
Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 100;
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Mouse embryonic cell EST 13-4 nucleotide sequence.
Embryonic stem cell; ESC; non-primate; mouse; EST; human; developmental gene; transgenic animal; reporter gene; ss.
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-4 NO. 0.061;
-2 NO. 20; Indels
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1; Mismatches
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27-NOV-1996; US-032510.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such diseases.
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Best Local Similarity 78.87
Matches 78; Conservative
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WPI; 98-322656/28.
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determining polymorphic forgaments are interested by the seating or phenotypic typing for disease

Claim 1: Page 219; 310pp: English.

Claim 2: Page 219; 310pp: English.

Claim 1: Page 219; 310pp: English.

Claim 2: Page 219; 310pp: English.

Claim 3: Page 310pp: English.

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                  as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       Human biallelic polymorphic DNA fragment EST98276a.
Polymorphism, biallelic; human: forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous non-human primate gene, in different cell types and/or at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hudson T. Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                     Score 65.4; DB 1; Length Pred. No. 0.09; 0; Mismatches 11; Indels
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06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                                                                                                                                                                                                                                                                                                                       0.2%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17/c
X12087 standard; DNA; 100 BP.
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                                                                                                                                                                                                                                                                                                                                                                   72; Conservative
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Best Local Similarity
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Sequence 100
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Hudson T. Lander ES, Wang DS.

NWI: 98-2865/4/25.

NWI: 98-2865/4/
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23012 GTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCTGAAGAAGGAGGATCGCTTGAGTC 23071
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Human biallelic polymorphic DNA fragment EST98276a.
Folymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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                                Gaps
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X12085;
30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276c.
                                                                                                             23072 CGGGAGTTCAAGAGCATCCTGGGCAACACACAGGGAGACCC 23110
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Pred. No. 0.18;
1; Mismatches 22;
                                                                                                                                              39 CAGGAGCTCAAGACCAKCCTGGGAAACATAGCAAGACTC 1
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06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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Sequence 100 BP; 21 A;
                                                                                                                                                                                                                                                                                                           X12087 standard; DNA; 100 BP.
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76.8%;
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Best Local Similarity 70.0.
To 76; Conservative
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WO9820165-A2.
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Gaps

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21; Indels

1; Mismatches Score 65; Pred. No.

0.28;

Query Match 0.2 Best Local Similarity 77.8 Matches 77; Conservative

DB 1; Length 100;

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

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Whisylated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity per determining polymorphic forms for use in e.g. forensics, paternity protecting or phenotypic typing for disease

Claim 1: Page 218; 310pp; English.

Claim 1: Page 218; 310pp; English.

Claim 1: Page 218; 310pp; English.

CC markers which have been isolated using the primers represented in the perpension of the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the et.g. forensics, paternity testing or form in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, cup as agammaglobulinemia, diabetes insipidus, Easch-Nyhan syndrome, hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, herefitzy spherocytosis, von Willebrand's disease, tuberous sclerosis, herefitzy spherocytosis, papearance (e.g. baldness, obesity), strength, speed, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such candurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid coppopalyzats of such diseases.

CC prophylaxis of such diseases.

Sequence 100 BP; 22 A; 25 C; 22 G; 30 T;
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30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276b.
Folymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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Polymorphism; biallelic; human; forensic; paternity testing; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGTCTTGCTATGTTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCC 60
                                    detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease Claim 1; Page 219; 310pp; English.
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Pred. No. 0.18;
1; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998.
05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES. Hudson T, Lander ES, Wang D; WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.2°
Best Local Similarity 76.8°
Matches 76; Conservative
                                                                                                                                                                                                                                                              05-NOV-1997; U20313.
06-NOV-1996; US-030455.
                                                                                                                 treatment; marker; ss
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WO9820165-A2.
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                  14-MAY-1998.
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X12086
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NEW WENT WAS A STATE OF THE STA
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markers which have been isolated using the primers represented in X09121-X10568. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17709 GGGICTTACTATGTTGCCCAGGCTGGTCTCAAACTCCTGGGCTTAAGTGATCCTCCTGCC 17768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9604 ICACTTGCCCTTGGCCTTGTGGTGACTCTCGGTCTTCTTAGGCAGAAGCACGGCCTGGAT 9663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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WPI; 94-035056/04.

New nucleic acid fragment encoding gene products - can be used clor genetic analysis and mapping
Claim 1; Page 64; 616pp; English.

Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q'6401-Q'7613), (B) an allelic variation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences exhibit no more than 90% homology to a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-1994 (first entry)
Human genome fragment. (Preferred)
Brain; placenta; bone marrow; genetic analysis; gene mapping; detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62.8; DB 1; Length 100;
Pred. No. 0.22;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 100;
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13-JUL-1992; GB-014857.
(MEDI-) MEDICAL RES COUNCIL.
Gross J, Hadfield KM, Howells D, Kelly M, Shaw D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY 17769 TCAGCCTCCCAAATTGTTGGGATTACTAGTGTGAGTCAC 17807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 C;
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Q76490;
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Local Sim
67;
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Matches
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DD Q7645
DT 23-Si
DE Humar
EWW detector
NWW detector
NWO 20-J4
PP 13-J1
PP 13-J1
PP 13-J1
PP MED 13-J1
PP GCOS
PP GCO
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double-stranded DNA (or its complementary strand or the corresp.

A single-stranded DNA) which comprises one of the 7837 "GS" sequences
glowe in 119001-T26837 and which is able to hybridise to part of
thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3559 TTTTTTTTTTTGAGACGGAGTCTAGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCACCATC 3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; Page 714; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3 'directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 TITGITIGITICAAACAGAGTGTCACTCTGTCACCCAGGCNGGAGTGCAANGGTGCAATC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
                                                                                                                                                                   WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3619 TIGGCICACTGCAAGCICTGCCTCCCGGGITTAIGCCAI 3657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 TCAGCINATIGCAAATICTGCCICCCAGGTTCAAGCGAT
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74.7%; Pred. No. 0.43;
:1ve 0; Mismatches
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T20743;
                                                                                                                                                                                                                                                                                          tissues
Claim 1; Page 1720; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene signature HUMGS01961.
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Matches 74; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                          11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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                                                                                                                                              Okubo K;
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WPI; 95-206931/27.
                                                                                                                                              Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The standard indicated acts as equality in the final golymorphic forms for disease

The stating or phenotypic typing for disease

PS Claim 1. Page 219; 310pp; English.

Calaim 1. Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic x10269-X12937 are human DNA fragments which contain biallelic polymorphic x10269-X12937 are human DNA fragments which contain biallelic polymorphic commarkers which have been isolated using the primers represented in commerce x00121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambliguity code. These fragments can be used in commethods for determining polymorphic forms in an individual for use in commethods for determining polymorphic forms in an individual for use in compact and a gagmmagolobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, caucha a gagmagolobulinemia diabetes insipidus, Lesch-Nyhan syndrome, cappercolemia, polycystic kidney disease, hereditary compact telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecte, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous contractive and paracteristics such as allonest and a paracteristics such as a paracteristics and a paracteristics contractive internity appendix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24415 TGTATTCCCAGCACTTT - - GGAGGCAGAGGCGGGCAGATCACTTGAGGTGGGGAGTTCGA 24472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism: biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cabcer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%; Score 62.2; DB 1; Length 108;
19.4%; Pred. No. 0.27;
.ve 1; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24473 GACTAGCCTGGCCAACATGATGAAACCCCATCTCTACTAAAAATACA 24519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell typing; abnormal cell function; ss. Homo sapiens. W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T24892/c
ID T24892 standard; cDNA to mRNA; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prophylaxis of such diseases.
Sequence 108 BP; 19 A;
                                                                                                                                                                      5/c
X12095 standard; DNA; 108 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hudson T, Lander ES, Wang D; WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.48;
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Best Local Similarity 79.4
Matches 85; Conservative
9664 GTTAGGAAGGACGC 9677
                                14 GTTGGGCAGGACGC 1
                                                                                                                                                                                                                                                                                                                                                                                                        treatment; marker; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09820165-A2.
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Gaps

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DB 1; Length 100; Indels

22 T;

25 G;

CDNA that

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1463 ATGGCGAAACCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGATGTGCTTC 1522 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 
untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 102 BP; 45 A; 26 C; 12 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'-end of mRNA by using poly(") as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene signature; messenger RNA, mRNA, relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ŧ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 6;
                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2%; Score 59.2; DB Best Local Similarity 75.3%; Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12193 TTGTTTCCCAGGCTGGAGTGCAATGGCGCGATC 12225
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 758-759; 2245pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77/c
720927 standard; cDNA to mRNA; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recognising different cell types. Sequence 103 BP; 22 A; 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okubo K;
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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T20927
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Claim 1. Page 2029; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp.
Couble-stranded DNA) which comprises one of the 7837 "GS" sequences
gluen in T19001-T26837 and which is able to hybridise to part of
the first of the comprises one of the 7837 "GS" sequences
couple-stranded DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed CDNA libraries prepared
from various human tissues; synthesis of CDNA was initiated from the
contranslated sequence is unique to a particular mRNAs ince the 3'-
untranslated sequence is unique to a particular mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13768 ITTTTTTTTTTTTGAGACAGAATTTTGCTCTGTGGCCCAGGCTGGGGTGCAGTGCCAAA 13827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 TTTTTTTTTTTTTAAAGACATGTTCTTACTCTGTGGCCCAGGCTGGAGTGCAGTGGTGGCCA 43
                                                                                                                                                                               13-NoV-1996 (first entry)
Human gene signature HDMGSOB452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%; Score 57.8; DB 1; Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 13828 TCTCGGCTCACTGCAACCTCTGCCTCCAGGGTTCTAGCAAT 13868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
1523 TGTGGTCCCAGCTACTCGGGAGGCTGAGGCTGAAGAATC 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 TCATAGCTCACTGTAACACCCAAACTCCTGGACTCAAGTGAT
                                       -
                    39 TGTAGCCACAGGTACTTGGGAGGTGGAAGTGGGAGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.2;
0; Mismatches
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                                                                                                                       T26213/c
ID T26213 standard; cDNA to mRNA; 103
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T25848;
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Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                          11-NOV-1994, J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                         Okubo K;
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                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                T26213;
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                                                                                                      RESULT
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Claim 1; Page 1942; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

Couble-stranded DNA) which comprises one of the 7837 "GS" sequences

given in T19001-T26837 and which is able to hybridise to part of

human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

circum various human tissues; synthesis of cDNA was initiated from the

circum various human tissues; synthesis of cDNA was initiated from the

circum various human tissues; synthesis of constructed sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

circum standard constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (sep. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for

recognising different cell types.

Sequence 84 BP; 33 A; 17 C; 15 G; 19 T;
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
MATSUBARA K, Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                           tissues
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0; Gaps Query Match

0.2%; Score 56.4; DB 1; Length 84;
Best Local Similarity 80.5%; Pred. No. 1.9;
Matches 66; Conservative 0; Mismatches 16; Indels ò

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17739 AAACTCCTGGGCTTAAGTGATC 17760

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22 GAACTCCTGGGCTCAAGGGATC 1

Search completed: June 14, 2000, 20:42:29 Job time: 27860 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq length: 110
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Wilson, R.
The Washu-Marck EST Project
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Insert Size: 721
High qality sequence stops: 68 Source: IMAGE Consortium, LLNL This
                                                                                                                                                                                                                                    3'); double-stranded cDNA was ligated to Eco RI adaptors IS AATTACTAGTAAT 3' and 5' ATTACTAGTAGT 3'), digested with Not I and Eco RI sites of the modified p1773 vector. Library constructed by Bob
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                                                  105 AGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGGTTGCGGTGAGCCAAGATCG 46
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                     61; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                       24630 CACCATTGCACTCCAGCCTGGGCAACAAGAGCAAAACTCTGTCTC 24674
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/organism="Homo sapiens"
/organism="Homo sapiens"
/b_xref="taxon:9606"
/clone="IMAGE:2377600"
/clone_llb="Barstead colon HPLRB7"
/sex="male"
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          Washington University School of Medicine
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Pred. No. 0.039;
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Contact: Wilson RK
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AA703692 ag81a10.r
AA3442529 zv68b02.r
A1991750 wt48e01.x
N49638 yv268e09.r1
AA835205 ak64h01.s
B61160 CIT-HSP-201
B61160 CIT-HSP-201
AA812141 ob48h02.s
AA44259 zv68b02.r
AA442529 zv68b02.r
AM750394 2822460.3
AA228795 RDC14E07.s
AA728795 RDC14E07.s
AA7260.3
                                                            T77382 Yd72h12.r1
AA158786 Zo63c11.r
AQ029590 RPC111-41
AAA44245 nc07a04.s
AA897366 am06h02.s
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N25299 yw52c09.s1
AQ544957 CITBI-E1-
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AW196212 xm06e06.x
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AQ544648 CITBI-E1-
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AQ062963 CIT-HSP-2
AA078003 7H12D08 C
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AA828124 od71a07.s
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B32951 HS-1016-A1-
                            A183283 yf19403.rl
A1832832 at72909.x
AA807640 nx08b05.s
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;

Butheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases i to 105)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project

Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133644.
Description
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                                                                                                                 AQ535244
AA703692
AQ386882
AA442529
AI991750
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clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 727 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 68.
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Pred. No. 0.066;
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Impublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151346.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Banall: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 103)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCAACCTCCACCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled germ cell tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.2; DB Pred. No. 0.06; 0; Mismatches
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/clone_11b="NCI_CGAP_GC3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.3%;
Best Local Similarity 92.4%;
Matches 97; Conservative
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ORIGIN
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Insert Size: 943
Source: IMAGE Consortium, LLNL This clone is available royalty-free
Source: IMAGE Consortium, info@image.llnl.gov)
for further information. Putative full length read
Insert Length: 943 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 109.
Location/Qualifiers
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Tab_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T77382 103 bp mRNA EST 15-MAR-1995 yd72h12.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:113831 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                           3734 AGTAGAGATGGGGTTTCACCGTGTTAGCCAGAATGGTCTCGATCTCTTGACCTTCTGATC 3793
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGTAGAGATGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTTGTGATC 61
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1 (bases 1 to 103)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Other_ESTS: yd72h12.s1
Contact: Wisson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
                                                                                                                                                                                                                                                                                                                         Length 103;
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/db_xref="tAxon:9606"
/clone="!WAGE:113831"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3794 CGCCTGCCTTGGCTTCCCAAAGTGCTGGGATTACACGTGTGA 3835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 87.6; DB 38;
Pred. No. 0.21;
0; Mismatches 9;
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The WashU-Merck EST Project
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                           0.3%;
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JOURNAL
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ZO63cll.rl Stratagene pancreas (#937208) Homo saplens cDNA clone IMAGE:591572 5' similar to contains Alu repetitive element; contains Alars PTR7 repetitive element; mRNA sequence.
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1 (bases 1 to 106)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
On bubblished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 119
Insert Length: 926 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               6077 TGAGAGTCTCACTCTCACTGCAACCTCCCCCTCCTATATTCAAGTGATTCTTTGCCTCA 6136
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                     103 TGAGAGTCTCACTCTCACTCGCAACCTCCCCTCCTATATTCAAGTGATTCTCTTGCCTCA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:4622958"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="liMaGE:591572"
/clone=lib="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (Kanamycin resistan)"
                                                                                                                                                                                                                               Length 103;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                   DB 21;
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                                                                                                                                                                                                                               Score 86.6; DB
Pred. No. 0.28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            6137 GCCTCCCGAGTAGCTGGGACTACAGGCGTGCAC 6169
                                                                                                                                                                                                                                                                                                                                                                                                                   43 GCTCCCGAGTAGCTGGGACCACAGGCGCCTAC 11
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Best Local Simi
Matches 89;
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AA158786/c
LOCUS
DEFINITION
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AA244245 110 bp mRNA EST 20-AUG-1997 nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence.
49 TACTAAAACTACAAAATTAGCCGGGCATGAAGGAGCATGACTGTAATC 1
                                                                                                                                              AA244245
AA244245.1 GI:1875104
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Eutherist Frimates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 tro 109)

Solden,K., Berry,K., Granger,D., Suh,E., Wible,C., Ge Jong,P. and Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

L Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Email: madamsetifian the human BAC library RPCI-11. For BAC (1916 Edejone) are derived from the human BAC library RPCI-11. For BAC (1916 Edejone) are derived from the human BAC library RPCI-11. For BAC (1916 Edejone) and Obtfalo.edu/ordering) or from BACPAC Resources (http://bacpac.med.buffalo.edu,ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                               AQ029690 109 bp DNA GSS 14-APR-1999
RPCI11-41F18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-41F18,
                                                                                                         12190 CTCTTGTTTCCCAGGCTGGAGTGCAATGGCGCGATCTTGGCTCACAGCAACCTCCGCCTC 12249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                              104 CICITGITICCCAGGCTGGAGTGCAAIGGTGCGACCTIGGCTCACTGCAACCTCCGCCTC 45
                                                                        ö
                                   Length 106;
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Pred. No. 0.42;
0; Mismatches 15; Indels
                                                                        Indels
                                                                                                                                                                                 12250 CCGGGTTCAAGCCATTCTCCTGCCTCAGCCTCCGGAGTAGCTGG 12293
                                                                                                                                                                                                     Score 84.8; DB 29;
Pred. No. 0.45;
0; Mismatches 12;
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/db_xref="taxon:9606"
/clone="RPCI-11-41F18"
/clone_lib="RPCI-11"
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AQ029690.1 GI:3274821
                                 0.3%;
llarity 88.5%;
Conservative (
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Best Local Similarity 86.24
Matches 94; Conservative
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Class: BAC end
                                                Similarity
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                                       Local S...
92;
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AQ029690/c
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//note="Vector: DAMP10; Site_1: Not1; Site_2: ECORI; 1st strand CDNA was primed with oligo(dTp17 on 50 ng of DNA was primed with oligo(dTp17 on 50 ng of DNA was primed with oligo(dTp17 on 50 ng of DNA was primed cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Knizman. I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
Tumor Gener Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Confact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@filh.gov
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illarity 85.5%; Pred. No. 0.42;
Conservative 0; Mismatches
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/clone_lib="NCI_CGAP_Pr1"
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/dev_stage="45 years old"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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4703 CATATCACCTGAGGTCAGGAGTTTGAGACCAGGCTGGCCAACATGGTGAAACCCTGTCTC 4762

0.3%; 86.2%;

109 CAGATCACCTGAGGTCAGGAGTTTGAGACCAGACAGGCCAACATGGTGAAACCCTGTATC 50

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4763 TACTATAAATATAAAATTAGCTGGGTGTGGTGCTGCATGCCTGTAGTC 4811

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 AA897366 110 bp mRNA EST 04-JAN-1999 am06h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466067 3' similar to contains Alu repetitive element;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
NCI-GGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                           Tunor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150764.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 834 Std Error: 0.00
Seq primer: -40m13 fwd. Err from Amersham
High quality sequence stop: 63.
Location/Qualiflers
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RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
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86.2%; Pred. No. 0.42;
tive 0; Mismatches 15; Indels
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/organism="Homo sapiens"
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/clone="IMAGE:1466067"
/clone="IMAGE:1466067"
/clone=11b="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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27 c 29 q 32 t
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Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: bbeetigr.org from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleter ded-jong med.buffalo.edu.clores may be purchased from BACPAC Research Genet cs (http://bacpac.med.buffalo.edu.cordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: T7
Class: BAC ends.
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1 (bases 1 to 10x.
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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RPCIII Human Male BAC Library"
27 c 27 q 18 t
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On Sep 12, 1996 this sequence version replaced gi:1397630.
Contact: Wilson RK
                                de Jong, P. and
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Contact: Shaying Zhao, William Nierman, Mark Adams
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Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
Venter,J.C.
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89.2%; Pred. No. 0.5;
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/db_xref="GDB:7621533"
/db_xref="taxon:9606"
/clone="RPOI-11:317H22"
/clone_lib="RPOI-11"
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ386882 110 bp DNA GSS 21-MAY-1999
RPCII1-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
Zhao,S., Adams,M.D., Nlerman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
4444 Forest Pain ...
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wstl.edu
Email: est@watson information information information information information information.
Seq primer: -26ml3 revi ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TTTTAGTAGAGGACGAGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGT 61
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Pred. No. 0.52;
0; Mismatches 13; Indels 0;
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Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Uniter Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Best Local Similarity 87.6%;
Matches 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 110)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kocaba,T., Lacy,M., Le,N., Lenon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL;
That vertor length reach
The vector to vector length is
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualiflers
                                                                                                                                                         /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCIII Human Male BAC Library"
1 26 c 38 g 20 t
                                                                                                                                                                                                                                                                                                                                                                                                                                           8191 GCCCGGCCGCGGTGCTCACGCCTGTAATCCCAGCACTTTGGTAGGCAGAGCTGGCGGA 8250
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997).
On Sep 12, 1996 this sequence version replaced gi:1400965.
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                         Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCGCTTGAGGTCAGGAGTTCAAGACCAGCCTGGACAACATGGTGAAAACC 110
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                            16; Indels
                                                                                                                                                                                                                                                                                                                                       Score 84.4; DB 106;
Pred. No. 0.49;
0; Mismatches 16;
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/db_xref="taxon:9606"
/clone="IMAGE:758763"
/organism="Homo sapiens"
/db_xref="GDB:7551267"
                                               /db_xref="taxon:9606"
/clone="RPCI-11-13414"
/clone_lib="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA442529.1 GI:2154407
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N49638 97 bp mRNA EST 14-FEB-1996
yv25e09.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:243784 5' similar to gb:x57138_rnal HISTONE H2B.2 (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: 17 High quality sequence stop: 1. Location/Qualifiers
  1 (bases 1 to 97)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Washu-Merck EST Project
Unpublished (1995)
Unpublished (1995)
Con Apr 14, 1993 this sequence version replaced gi:693230.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                       N49638 T GI:1190804
                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Matches 88; Conserv
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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
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A1991750 GI:5838578
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 106)

NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
Twitional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133359.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Tel: (301) 406-1550

Tel: (301) 406-1550

Tel: (301) 406-1550

Tel: (301) 406-1550
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llarity 86.1%; Pred. No. 0.55;
Conservative 0; Mismatches 15; Indels
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Pred. No. 0.62;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2510712"
/clone=lib="NCI_CGAP_Pan1"
/tisue_type="adenocarcinoma"
/lab_host="DH10B"
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High quality sequence stop: 62.
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86.8%;
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                                                                                                                                                                                        Length 97;
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                                                                                                                                                                                         DB 25;
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90.7%; Pred. No. 0.71;
ive 0; Mismatches
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Search completed: June 14, 2000, 15:22:36 Job time: 9923 sec

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: O7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/260,190
FILING DATE: I5-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leander, Leona L.
REGISTRATION NUMBER: D-0021.3E
FELECOMMUNICATION INDRER: D-0021.3E
TELEFAX: 415-435-20127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71.4; DB 4;
Pred. No. 5.2e-07;
US-08-340-426D-91
US-08-450-673C-91
BC-08-5-1711A-91
US-08-340-426D-60
US-08-454-557C-60
US-08-450-673C-60
US-08-454-557C-92
US-08-340-426D-92
US-08-340-426D-57
US-08-340-426D-57
US-08-454-557C-57
US-08-454-557C-57
US-08-454-557C-57
US-08-454-557C-60
US-08-454-557C-60
US-08-454-557C-60
US-08-454-557C-60
US-08-454-557C-60
US-08-454-557C-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/08481658B
Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ATTLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
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CITY: Tiburon
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US-08-481-658B-65
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-486-756A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-486-73C-70
US-08-450-73C-70
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US-08-450-673C-91
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US-08-440-426D-91
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US-08-450-673C-69
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 110
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US-08-486-756A-65
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Pred. No. 5.2e-07;
0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              21; Indels
                                                                                        3780 ITGACCTICIGATCCGCCTGCCTTGGCTTCCCAAAGTGCTGGGAT 3824
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0; Mismatches
                                                                                                                                                                                                                                       APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                US-08-477-504A-65; Sequence 65, Application US/08477504A; Sequence 65, Application US/08477504A; Setent No. 5972353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 80.0%;
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TYPE: nucleic acid
STRANDEDNESS: single
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84; Conservative
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US-08-477-504A-65
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3720 TTTTTTTTTTTTAGTAGAGATGGGGTTTCACCGTGTTAGCCAGAATGGTCTCGATCTC 3779
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0.2%; Score 71.4; DB 4; Length 105;
Best Local Similarity 80.0%; Pred. No. 5.2e-07;
Matches 84; Conservative 0; Mismatches 21; Indels
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APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3780 IIGACCTICIGATCCGCCTGCCTTGGCTTCCCAAAGTGCTGGGAT 3824
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Sequence 65. Application US/08486756A
Patent No. 5891711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
CORRESPONDENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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Patent No. 5989838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: FlORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-C
TELECOMMUNICATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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US-08-486-756A-65
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RESULT

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; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO ; ANTI-SENSE: NO US-08-787-739-65
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INFORMATION FOR SEQ ID NO: 65:
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LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 80.0$
Matches 84; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                    COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRICA PAPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leader, Leona L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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Fatent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00.
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-435-2034
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                 COMPUTER READABLE FORM:
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STATE: California
California
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Best Local Similarity
Matches 84; Conserva
                             USA
                                                               94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-08-485-862B-65
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                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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3720 TTTTTTTTTTTAGTAGATGGGGTTTCACCGTGTTAGCCAGAATGGTCTCGATCTC 3779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3780 TIGACCTICTGATCCGCCTGCCTTGGCTTCCCAAAGTGCTGGGAT 3824
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Pred. No. 5.2e-07;
0; Mismatches 21;
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Sequence 65, Application US/08481658B
Sequence 65, Application US/08481658B
Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Bastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STREET: California
COURTER OF SEQUENCES
COURTER OF SEGUENCES

APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-UN-1995
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1395 ATCTCAGCACTTTGGGAGGCTGAGG-GCACAGATCACGAGGTCGGGAGTTTGAGACCAGC 1453
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CURRENT APPLICATION DATA: US/08/486,756A
APPLICATION NUMBER: US/08/486,756A
FILING DATE: US/08/101/1995
CLASSIFICATION A 424
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1454 CTGGCCAATATGGCGAAACCCTGTCTCTACTAAAAATACAAAA 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 CTGGCCAATATGGTGAAACCCTGTCTACTACAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 69.6; DB 4;
85.6%; Pred. No. 1.3e-06;
vative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
  NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/CDOCKET NUMBER: D-0021.3D
TELEPRONE: 415-435-2034
TELEPHONE: 415-435-0727
INPORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lauder, Leona L.
REGISTRATION INUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.v.
Rest Local Similarity 85.v.
Rest Local Similarity 85.v.
                                                                                                                                                                                     LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-486-756A-65/c
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US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

0.2%; Score 69.6; DB 4; Length 105;
Best Local Similarity 85.6%; Pred. No. 1.3e-06;
Matches 89; Conservative 0; Mismatches 14; Indels 1
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                            CLASSILLATION: 4.4.
PRIOR APPLICATION 10474.

APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 0-0021.3E
REFERENCE/DOCKET NUMBER: 0-0021.3E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAK: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE: 105 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94920
COMPUTER READABLE FORM: •
MEDIOM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-477-504A-65/c
; Sequence 65, Application US/08477504A
; Patent No. 5972353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE:
US-08-481-658B-65
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1;

Length 105;

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COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TANGENT INFORMATION:
                                                                                           APPLICANT: Zavada, Jan
APPLICANT: Zastorekova, Silvia
APPLICANT: Zastorekova, Silvia
APPLICANT: Zastorekova, Silvia
APPLICANT: Zastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 359 Pine Street, Suite 610
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMONICATION:
TELEPHONE: 415-981-2034
TELEPHONE: 415-981-2034
                                                                                                                                                                                                         RESULT 10
US-08-787-739-65/c
Sequence 65, Application US/08787739
Patent No. 6027387
GENERAL INFORMATION:
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                               1; Gaps
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                                                                                                                                      Query Match 0.2%; Score 69.6; DB 4; Length 105; Best Local Similarity 85.6%; Pred. No. 1.3e-06; Matches 89; Conservative 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Flow PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/477,504
FILING DATE: 107-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/ACENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                       US-08-485-862B-65/C
Sequence 65, Application US/08485862B
Sequence 65, Application US/08485862B
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..rowdGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                  2
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US-08-485-862B-65
                                               ; ANTI-SENSE:
US-08-486-756A-65
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GENERAL INFORMATION:
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US-08-340-426D-70
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US-08-450-673C-70
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APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2840 GCCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTAGT 2899
                                                                                                           1395 ATCTCAGCACTTTGGGAGGCTGAGG-GCACAGATCACGAGGTCGGGAGTTTGAGACCAGC 1453
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                                                                   Gaps
                                                                                                                                                       105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
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                   Length 105;
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                                                                14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                       1454 CTGGCCAATATGGCGAAACCCTGTCTTCTACTAAAATACAAAA 1497
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ZIP: 20005-3934

COUNTER READABLE FORM:
MEDIUM TYER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
INFORMATION FOR EQ. ID NO: 70:
SEQUENCE CRARACTERISTICS:
LENGTH: 78 base pairs
LENGTH: 78 base pairs
STRRANFESS: hoth
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                0.2%; Score 69.6; DB 5;
85.6%; Pred. No. 1.3e-06;
tive 0; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                              Sequence 70, Application US/08454557C Patent No. 5830670
                                                                Conservative
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                Query Match
Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                             US-08-454-557C-70
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Patent No. 594888
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
TITLE OF INVENTION: of Alzheimer's Disease
TITLE OF INVENTION: of Alzheimer's Disease
TORRESPONDENCE: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2840 GCCCAGCTAATTTTTTTTTTTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTAGT 2899
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                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILLING DATE: 14-NOV-1994
CLASSIFICATION: 435
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58.6; DB 4;
Pred. No. 0.00029;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0609.3840002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION UNDHER: 36,203
REPERENCE/DOCKET UNDHER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202) 371-2600
TELEFRAN: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDENESS: both
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%;
Best Local Similarity 87.7%;
Matches 64; Conservative
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Sequence 70, Application US/08454557C
Fatent No. 5830670
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                2840 GCCCAGCTAATTTTTTTTTTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTAGT 2899
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                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY.

COUNTRY.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OOFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,557C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 514
                                                                                                    Query Match 0.2%; Score 58.6; DB 6; Best Local Similarity 87.7%; Pred. No. 0.00029; Matches 64; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.2%; Score 57.2; DB 3; Best Local Similarity 83.3%; Pred. No. 0.00059; Matches 65; Conservative 0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDENESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1495 AAATTAGCTGGGCATGGT 1512
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                                                                                                                                                                                                                                                                                                                   both
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US-08-454-557C-70/c
              ; TOPOLOGY: t
PCT-US95-17111A-70
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US-08-454-557C-70
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 70, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.6; DB 4; Length 78;
Pred. No. 0.00029;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION NUMBER: US/08/450,673C
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107 OCCUPANTION:
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TERNOTH: 78 base pairs
TERNOTH: 78 base pairs
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ludwig, Steven R.
REGISTAATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPRAN: (202) 371-2600
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%;
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Best Local Similarity 87.7%
Matches 64; Conservative
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
PCT-US95-17111A-70
                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-450-673C-70
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Gaps

Search completed: June 14, 2000, 20:28:41 Job time: 27251 sec

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                                                                                                            June 14, 2000, 20:22:29; Search time 17971.3 Seconds (without alignments) -1569.830 Million cell updates/sec
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29001
1 ATATCAACAAAACACACAT.....TTAGCAGCACAAGGTAGGGT 29001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  882769 seqs, -486395729 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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gb_in2:*
em_ba1:*
em_ba2:*
em_hum3:*
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gb_htg3: *
gb_htg4: *
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gb_htg6: *
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Maximum DB seq length: 110
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Perfect score:
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gb_htg9:*
gb_htg10:*
gb_htg11:*
gb_htg12:*
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gb_htg7:*
em_htg1:*
em_htg2:*
em_htg3:*
em_htg3:*
                       gb_pl3:*
gb_pr5:*
gb_htg8:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	304 sy899	Human	03 Human	Human C	304 Human	M87896 Human Carci	Human	Human	Human	Human		⊂ .	M87900 Human carci	Human ]	789 Human sed	Human C	M87924 Human carci		67803 Human	Human tamil	Human	U6/807 Human small	Human 10w	6 Human sma	00 Human	Human		Human	Human C	Human	~	Human	Human	Human	SYS Human STS	643535 WIAF-2393-5	To million of	<b>,</b>	224 number 213	3263 Human GAL	7 A T
91	G31304	HSLDLRN2 HSLDLRN2	HSU67803	HUMALCE162	HSU67804	HUMALCE221	HSLDLRD1	HSLDLRD2	HSLDLRD1	HSLDLRD2	HSLDL112	HSU6/808	HUMALCE43	HUMLDLRFL	HS81C8R	HUMALCE272	HUMALCE162	HSLDL112	HSU67803	HUMLDLRDJ	HSBICBR	HSU6/80/	HIM DI BY 2	HSU67806	HUMALCE43	HUMGALNSA	HUMD1D03M5	HUMD1D03M5		HSU6/806	5/9560	HSU6/8U8	HUMUTBI64A	מ מ	HUMUTUSIA	G43333	nombane ne	G32014 HIMITER 164 8	,	HUMGALNSA	
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                                                                                                                                                                                              Clone-contig and STS maps of the hereditary hemochromatosis region on human chromosome 6p21.3-6p22 Genome Res. 7 (5), 457-470 (1997)
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                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eulberia; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)

Lauer, P., Meyer, N.C., Prass, C.E., Starnes, S.M., Wolff, R.K. and
                                     sy899g1-19 Human (A.Gnirke) Homo sapiens STS genomic, sequence
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Pred. No. 4.4e-08;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                   degrees C for 20 seconds degrees C for 45 seconds degrees C for 60 seconds
                                                                                                                                                                                                                                                                                          Contact: Andreas Gnirke
Mercator Genetics, Inc.
4040 Campbell Ave, Menlo Park CA, 94025, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MJ Research PTC-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human (A.Gnirke)"
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each 0.8 uM
each 200 uM
0.05 units/ul
12 ul
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                                                                                                                                                                                                                                                                                                                                  Email: gnirke@mercator.com
Primer A: GTCCCCAAAGAATATAAATGAG
Primer B: AGGGCACAGTGGGGAAG
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50 mM
10 mM
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Matches 95; Conservative
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PCR Profile:
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhii; Hominidae; Homo.

1 (bases 1 to 108)
HORSTHERNEY, B., Belsiegel, U., Dunning, A., Havinga, J.R., Milliamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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     20-MAY-1992
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
                                                                                                 Alu repetitive sequence; low density lipoprotein receptor
HSLDLRN2 108 bp DNA PRI 20-MAY-
Human LDL-receptor gene intron 14 fragment (normal gene).
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 1.5e-07;
0; Mismatches 9;
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/db_xref="taxon:9606"
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Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitted (22-407-1996) Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10907 TAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCA 10966
                                                                                                       7174 AAAAAATTAGCCGTGCATGGTGGCATGCGCCTGTAGTCTCAGCCACTTGGGAGGCTGAG 7233
                                                                             Gaps
                                                                                                                         Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 108)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M. A. and Deininger, P. L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
                                                                                                                                                                                                                                                                                01-AUG-1997
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                                              Length 108;
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Homo sapiens male embryo carcinoma cDNA to other RNA.
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                                                                                                                                                                     7234 GCAGGAAAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAG 7281
                                                                                                                                                                                     61 GCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAG 108
                                                                            Indels
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                                        Score 90.4; DB 10;
Pred. No. 2.5e-07;
0; Mismatches 11;
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Human small cytoplasmic Alu transcript.
U67803
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/db_xref="taxon:9606"
/clone="TscAlu2"
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/rpt_type=dispersed
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/note="scAlu"
                                           Query Match 0.3%;
Best Local Similarity 89.8%;
Matches 97; Conservative
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M87924.1 GI:174871
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TITLE
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitsed (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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1 (bases 1 to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Best Local Similarity 90.3%; Pred. No. 1.1e-06;
Matches 93; Conservative 0; Mismatches 10; Indels
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94.7%; Pred. No. 1.1e-06;
tive 0; Mismatches 5; Indels
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Human small cytoplasmic Alu transcript.
U67804
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                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_cell_line="WrerazD1"
/dev_stage="embryo"
/sex="male"
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/db_xref="taxon:9606"
/clone="TscAlu3"
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30 c 35 g 1
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/rpt_type=dispersed
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Matches 90; Conservative
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/tissue_type="carcinoma"
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1 (bases 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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1 (bases 1 to 103)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. (1992) In press

Location/Qualifiers
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10908 AGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCAC 10967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATCTGCCTGTAATCCCAGCTACACGGAAGCTAAGGCAGGAAATCGCTTGAACCCGGGA 60
                    95 AAAGACGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTTGTGATCCTC 36
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
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Pred. No. 2.2e-06;
0; Mismatches 11; Indels (
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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                                                                      10968 CCGCTTTGGCCTCCCAAAGTGCTGGGATTACAGGC 11002
                                                                                         CCGCTTTGGCCTTCCAAAGTGCTGGGATTACAGGC 1
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/db_xref="taxon:9606"
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27 c 33 g 1
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/db_xref="taxon:9606"
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/dev_stage="embryo"
/sex="male"
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/sex="male"
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M87896.1 GI:174874
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Best Local Similarity
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AUTHORS
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Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSLDLRD1 108 bp DNA PRI 20-MAY-1992
Human LDL-receptor mutated gene with intron 12 deletion junction.
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                                                                                                                                                                                                     5440 CTGGAGTGCAATGGCGGGATCTCGGCTCACCGCAACCTCTACCTCCCAGGTTCAAGCAAT 5499
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 108)
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                                                                                             Score 84; DB 9; Length 103
Pred. No. 4e-06;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                     TCTCCTGCCTTAGCTTCCCGTGTAGCTGGGATTACAGGCA 4
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Pred. No. 3.6e-06;
0; Mismatches 13
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33 g
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Best Local Similarity 90.0°
Matches 90; Conservative
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
                                                                                                                                                                      Williamson R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 108)
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                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrihii; Hominidae; Homo.
1 (bases 1 to 108)
                      Alu repetitive sequence; low density lipoprotein receptor
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                                                                                                                                                  Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia
Bur. J. Biochem. 164 (1), 77-81 (1987)
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See X0520 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
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                                                                                                        /note="deletion junction region intron 12/ intron 15" 40 \, \mathrm{c} 20 q 28 t
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Alu repetitive sequence; low density lipoprotein receptor.
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Pred. No. 6.1e-06;
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Pred. No. 6.1e-06;
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FEATURES
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1 (bases 1 to 108)
Horsthemke, B., Beisisele, U., Dunning, A., Havinga, J.R., Millamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia By 161901
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                 HSLDL112 108 bp DNA PRI 20-MAY-1992 Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
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Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
1. .108
/organism-"Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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                                                                                                           Alu repetitive sequence; low density lipoprotein receptor repetitive sequence.
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Pred. No. 1.2e-05;
0; Mismatches 16; Indels
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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Human small cytoplasmic Alu transcript.
U67808
U67808.1 GI:2289922
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38 c 20 g 29 t
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/db_xref="taxon:9606"
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Best Local Similarity 85.0%;
Matches 91; Conservative
                                                       density lipoprotein.
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) in press
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ilarity 84.0%; Pred. No. 3.8e-05;
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                                                                                                                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-726837 and which is able to hybridise to part of human gromatc DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed as as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequence) as means of diagnosing abnormal cell function or for crecognising different cell types. 25 G; 25 T;
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                                                             Human gene signature HUM4506998.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

W09514772-A1.
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Pred. No. 0.041;
0; Mismatches 21; Indels
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Claim 1; Page 1720; 2245pp; Japanese.
                         T24892 standard; cDNA to mRNA; 100
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Human gene signature HUMGS02180.
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Best Local Similarity 78.8
Matches 78; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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WPI; 95-206931/27.
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WPI; 95-206931/27.
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Testing polymorphic forms for use in e.g. forensics, paternity determining polymorphic typing for disease

Esting or phenotypic typing for disease

Claim 1: Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in CX 030121-X10268 and the been isolated using the primers represented in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the appropriate IUPAC-IUB ambiguity code. These fragments can be used in the appropriate IUPAC-IUB ambiguity code. These fragments for use in the complex for determining polymorphic forms in an individual for use in the appropriate IUPAC-IUB ambiguity sesting or for phenotypic typing for diseases complexed as agammaglobulinemia, diabetes inspiduous, lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familiah hypercholesterolemia, polycystic kidney disease, thereforest, hereditary compensation of the partors and complexed autoimmune diseases, inflammation, cancer, diseases of the nervous such autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longerity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular
                                                                                                                                                             Care A single-stranded DNA) with comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is calemed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-ond of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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Polymorphism, biallelic; human; forensis; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid segments from the human genome - used for
preparing cDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                          reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9954 CTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATC 9993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i; DB 1;
o. 0.062;
for diagnosis of abnormal cell function, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                Page 758-759; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 66;
78.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WHED ) WHITEHEAD INST BIOMEDICAL RES. Hudson T, Lander ES, Wang D; WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X12095 standard; DNA; 108 BP
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06-NOV-1996; US-030455.
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Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9820165-A2.
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Matches

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                                                                                                                      X12087 standard; DNA; 100
                                                                                                                                                                         30-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis of
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
WO9820165-A2.
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                                                                           RESULT
X12087/c
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Why: 98 - 28694/25.

Why: 98 - 28694/26.

Why: 98 - 2864/26.

Why: 98 - 2864
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                                                                                                                                                                                                                                          21852 TGTATTTTAGTAGAGGGGGTTTCACCATGTTGGTCAGGCTGGTCTGGAACTCCTGAC 21911
treatments. The isolated polymorphic nucleic acid used to produce medicaments for the treatment or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human biallelic polymorphic DNA fragment EST98276b.
Polymorphism: biallelic; human: forensic; paternity testing; disease; detection: phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                  Gaps
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                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                          21912 CTCAGGTGATCTGCCCACCTCAGCCTCCC-AAAGTGCTGGGATTACAG 21958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 100;
                                                                                                                                             Score 65.2; DB 1; Length 10
Pred. No. 0.082;
1; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                      61 TTCAAGTGATCCGTCTGCCTTGCCTCCCAAAAGTGCTGGGATTATAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
                                                                           37
                                                                           28 G;
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Pred. No. 0.12;
1; Mismatches
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                                                                         ΰ
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     drugs or therapeutic treatments.
                                                  prophylaxis of such diseases.
Sequence 108 BP; 19 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X12086 standard; DNA; 100 BP
                                                                                                                                               0.2%;
                                                                           19 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 77.6
Matches 76; Conservative
                                                                                                                                                                                          87; Conservative
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06-NOV-1996; US-030455.
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                         segments can also be
                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                               Query Match
Best Local
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determining portynologic forms for use in e.g. Forensics, paternity

testing or phenotypic typing for disease

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

X10269-X12937 are human DNA fragments which contain biallelic polymorphic

markers which have been isolated using the primers represented in

X09121-X10268. The base occupying the polymorphic site is indicated by

the appropriate IUPAC-IUB ambiguity code. These fragments can be used in

methods for determining polymorphic forms in an individual for use in

e.g. forensics, paternity testing or for phenotypic typing for diseases

such as agammaglobulinmenta, diabetes insiphidus, Lesch. Nyhan syndrome,

muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial

spherocytosis, on Willebrand's disease, tuberculs sclerosis, hereditary

contoner, osteogenesis imperfects, acute intermittent porphyria,

autoimmune diseases, inflammation, cancer, diseases of the nervous

system, infection by pathogenic miscroorganisms, and characteristics such

as longevity, appearance (e.g. baldness, obesity), strength, speed,

endurance, fertility, and susceptibility or receptivity to particular

drugs or therapeutic treatments. The isolated polymorphic nucleic acid

system, since the streatments. The isolated polymorphic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22822 GAGGCTCTTGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGAGGATGGCTTGAGCC 22881
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Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                            Human biallelic polymorphic DNA fragment EST98276a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity
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Pred. No. 0.
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05-NOV-1997. U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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78.1%;
BP.
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ID X12085 Standard; DNA; 100 BP X12085 C
X X12085;
DT 30-MAR-1999 (first entry)
DE Human biallelic polymorphic
KW Polymorphism; biallelic; hum
W detection; phenotypic typing
KW autoimmune disease; cancer;
KW treatment; marker; ss.
OS Homo saplens.
PN W09820165-A2.
PD 14-MAY-1998.
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4363 CAGGAGTTCAAGACCATTTTGGGCAACATAGCAAGTCT 4400

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Matsubara K,
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                                                                                    determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease

Tain 1. Page 218; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic x10269-X12937 are human DNA fragments which contain biallelic polymorphic x10269-X12937 are human DNA fragments which contain biallelic polymorphic of markers which have been isolated using the primers represented in CC x09121-X10268 The base occupying the polymorphic stre is indicated by cc the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in CC e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, cc e.g. forensics, paternity diseases, hereditary spherocytosis, von Willebrand's disease, hereditary companies, osteogenesis in morefected, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such conting the propertity appearance (e.g. baldness, obesity), strength, speed, condurance, fertility, and susceptibility or receptivity to particular conting also be used to produce medicaments for the treatment or prophylasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGCTCTTGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGAGGATGGCTTGAGCC 22881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 GTGACTCACACCTATAATCCTGGCACTTTRGGAGGCTTAGGAAGGAGGAGTTGTTTGAAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                         Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63.6; DB 1; Length 100;
Pred. No. 0.14;
1; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22882 CAGGAATTCAAGACCAGCCTGGGAAACATAGGGAGA 22917
                                                                                                                                                                                                                                                                                                                                                                                                                                             22 G;
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(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               25 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T24892 standard; cDNA to mRNA; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis of such diseases. Sequence 100 BP; 22 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.2%;
78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               22 A;
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 75; Conserv
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05-NOV-1996
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T24892
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Claim 1; Page 2029; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

Gouble-stranded DNA, which comprises one of the 7837 "GS" sequences

Gouble-stranded DNA, which comprises one of the 7837 "GS" sequences

Gouple-stranded DNA, which comprises one of the 787 "GS" sequences

C given in T19001-T28837 and which is able to hybridise to part of

Numan genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed CDNA libraries prepared

C from various human tissues; synthesis of CDNA was initiated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

untranslated sequence is unique to a particular mRNAs in almost

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS.

Sequences) as a means of diagnosing abnormal cell function or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6312 ATCGCTTGAACCTGGGAGGCGGAGATTGCAGTGAGCCGAGATCGCACCACCACGCACTCCAG 6371
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNNA hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATCGCTTGAACCTGGGAGGCAGAATTTGCAATNAGCTGAGATTGCACTTGCACTCCNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frequency;
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Human gene signature HUMGSOB452.

Homen gene signature, messenger RNA; mRNA; relative abundance; frequency fundan; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 95-206931/27.

Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62.4; DB 1; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6372 CCTGGGAGACAGGCGGGGCTCCGTCGGAAAAAAAA 6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ccredergacagagagacactcrerrrgaaacaaacaaa 100
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0; Mismatches
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Pred. No. 0.2;
0; Mismatches
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Sequence 103 BP; 33 A; 21 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T26213 standard; cDNA to mRNA; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 75.8 Matches 75; Conservative
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Best Local Similarity 76.2
Matches 77; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okubo K;
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W09514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                              A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences of jiven in 719001-726837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-entranslated sequence is unique to a particular mRNAs instance of its constructed so as to reflect accurately the relative abundance of different mRNAs in the particular issue from which it, was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 18 A; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10945 GATCTCCTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGATTACAGGCGT 11004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
                                                                                        Human gene signature HUMGS09078.
Gene signature: messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; Humo sapiens.
Human sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GATCTCCTGACCTCGTCATCCGCCCGTNTCGGCCTCCCATAGTGCTGGGNTTACAGGCAT
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Pred. No. 0.23;
0; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY 11005 GAGCCACCGTGCCCGGCCTACTTCACTTTCATTAAAA 11045
            15835 TCTCAGCTCACTGCAACCTGCACCTCCTGGGTTCAAGGGAT 15875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAGCCACCACGCCGGCTGTTTATTTCTTATAACTGTACA 101
                          42 TCATAGCTCACTGTAACACCCAAACTCCTGGACTCAAGTGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T20927 standard; cDNA to mRNA; 103 BP
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Human gene signature HUMGS02180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%;
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Best Local Similarity 75.2
Matches 76; Conservative
                                                                                                                                                                                                                             01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                   Okubo K;
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11-NOV-1994; J01916.
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                                                                                                                                                                                                                                                                                                   Matsubara K,
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T20927
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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer, since the 3'-end of mRNA in the particular mRNAs mass decises, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.9
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Homo sapiens.
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                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 0.46;
0; Mismatches 25; Indels
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Human gene signature HUMGS08084.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
                                                                                    Matsubara K, Okubo K;
WPI; 95-206931/27.
(MATS/) MATSUBARA K. (OKUB/) OKUBO K.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                           is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. 23 G; 23 G; 28 T;
    constructed so as to reflect accurately the relative abundance of
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reflects relative abundance of corresp. mRNA in specific human tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1996 (first entry)
Human gene signature HUMGS09078.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; eall typing; abnormal cell function; ss.
is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
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                                                                                                                                                                                      DB 1; Length 91;
                                                                                                                                                                                                                             20; Indels
                                                                                                                            28 G;
                                                                                                                                                                                      0.2%; Score 59.4; Di
Similarity 77.5%; Pred. No. 0.6;
9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       15847 GCAACCTGCACCTCCTGGGTTCAAGGGAT 15875
                                                                                                                                                                                                                                                                                                                                                                                                30 TGAACCNCTGCCTCCTAGGCTCAAGTGAT 2
                                                                                                    recognising different cell types.
Sequence 91 BP; 18 A; 22 C;
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATE/) MATESBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okubo K;
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A single-stranded DNA for its complementary strand or the corresp.

C double-stranded DNA, which comprises one of the 7837 "62" sequences gloven in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) c sequences were obtained from 3'-directed CDNA ibraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-end of mRNA by using poly(") as the sole primer since the 3'-end of mRNA by using poly(") as the sole primer since the 3'-end of mRNA in the particular mRNA specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS csequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15769 TTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCACTCTATCACCCAGGCTGGAGTGCAGTG 15828
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Human gene signature HUMGS07131.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.
                                                                                                         Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                        WPI; 95-206931/27. Identifying quene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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71.0%; Pred. No. 0.
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T25009/c
ID T25009 standard; cDNA to mRNA; 108
AC T25009;
                                                               07-NOV-1996 (first entry)
Human gene signature HUMGS07131.
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                                                                                                                                                                                                                                 11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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Matches 76; Conserv
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which is one of the 7837 "63" sequences double-stranded DNA) which comprises one of the 7837 "63" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular mish shows the sole primers and probes derived from the GS determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 34 A; 25 G; 15 T;
Matsubara K, Okubo K;
WPI: 95-206931/27.
Identifylng gene signatures in 3'-directed human cDNA library - e.g.
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                          tissues
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ö Gaps 0; Query Match 0.2%; Score 57.8; DB 1; Length 108; Best Local Similarity 72.5%; Pred. No. 1; Matches 74; Conservative 0; Mismatches 28; Indels C

7242 ATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATCATGCCACTGCATTCCAG 7301 2 ATCGCCTGAGCCCATGAGGCCAAGGCTGCAGTGAGCCATGATCAGGCTCAG 61 ô g

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62 CCTGAGTGACAGGAAGACCCTGTTGAAAACAACAACAACA 103

Search completed: June 15, 2000, 05:38:04 Job time: 59995 sec

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1 ATATCAACAAAACACACAT......TTAGCAGCACAAGGTAGGT 29001
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

    nucleic search, using sw model

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FEATURES	BASE COUNT ORIGIN Query Matc Best Loca Matches	QY 10897 G;  DD 1 G;  QY 10957 TC  QY 10957 TC  DD 61 TC  EBSULT 2  B174.4/C  LOCUS  DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM TATHORS TITLE JOURNALL COMMENT
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AA24309 AI32832 AA703692 AA703692 AQ284176 AQ28426 AQ28426 AQ285244 AA078003 AA078003 AA078003 AA078003 AA078003 AA8914 AQ265749 AQ0004934 AA897366 AQ062963 AA897366 AQ082107 AQQ82107 AQQ82107 AAA442529	AA812141 AQ321855 AW083640 AA564832 AA654562 AQ584425	B65160 H67040 AW250394 AA564832 AA534922 AG37292 AG37292 AG485214 AA485214 AA381369 AG485214 AA381369 AG240182	mRNA NT2 neuronal pr 7 3' similar to nt LTR1 repetit cordata; Craniat tarrhini; Homin Bowles, L., Dubu Lacy, M., Le, N. chellenberg, K., chellenberg, K., oject
330 611 105 37 37 37 37 37 37 37 37 37 37 37 37 37	38 1105 35 36 108	84 24 779 35 1109 1107 33 108	bp 36446 56446 51646 73869 73869 7387 74. 74. 74. 74. 74. 75. 76. 76. 76. 76. 76. 76. 76. 76
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			RESULT 1 A243009 LOCUS DEFINITION ACCESSION KEYWORS SOURCE ORGANISM TITLE JOURNAL

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/db_xref="cb16:4467"
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/clone="IMAGE:66467"
/clone="IMAGE
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345K2.TVB CIT978SKA1 Homo sapiens genomic clone A-345K02, genomic
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feat: 314 286 1810
Fax: 316 286 1810
Fa
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AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
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1 (bases 1 to 106)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Marthi,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL;
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the modified pT/T3 vector. Library constructed by Bob
Barstead."
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On Sep 12, 1996 this sequence version replaced g1:1397630.
Contact: Wilson RK
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E 1 (basea 1 to 105)

E 1 (basea 1 to 105)

Krizman, D., Rucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Mashu-NCI human EST Project

L Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133644.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810
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/gex="Female"
/cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_l: HindIII; Site_2: HindIII;
CalTech Human BAC Library Al"
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40UP from Gibco.
Location/Qualifiers
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                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
                                                                                                                                              /clone="A-345K02"
/clone_lib="CIT978SKA1"
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Homo sapiens
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalla;
Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3-21
Class: BAC ends.
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1 (bases 1 to 103)

2 hao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
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Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                         Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Addical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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89.9%; Pred. No. 0.33;
tive 0; Mismatches 11;
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  AQ028426.1 GI:3268648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Conteact: Mark Adams
Conteact: Mark Adams
Conteact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: medadams@tigr.corg
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.corg/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3-21
Class: BAC ends.
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
1 0 c 34 g 17 t
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CTT-HSP-2313G15.TF CIT-HSP Homo sapiens genomic clone 2313G15,
genomic survey sequence.
AQ028426
                                                                                                                                                                                                                                AQ264176 106 bp DNA GSS 27-OCT-1998
CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2,
  Query Match

0.3%; Score 91.6; DB 105; Length 106;
Best Local Similarity 91.5%; Pred. No. 0.32;
Matches 97; Conservative 0; Mismatches 9; Indels 0;
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                                                                     QY 10960 TGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTG 11005
                                                                                             61 TGATCTGCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTG 106
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/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
/sex="male"
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/cell_line="HeLa cell line; ATCC"
/lab_host="E. coli strain DH5 alpha"
/note="Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT).
From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Con Apr. 14, 1993 this sequence version replaced gi:693433.

Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bullding 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6265 TGGTGTGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGGGGCAGGAGAATCGCTTGAACCT 6324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA078003 105 bp mRNA EST 24-SEP-1999
7H12D08 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone
7H12D08, mRNA sequence.
AA078003 GI:1837477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 TGGTGTGTGCCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATCACTTGAACCT 48
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6325 GGGAGGCGGAGATTGCAGTGAGCCGAGATCGCACCACCGCACTCCAG 6371
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    ity sequence stop: 87. Location/Qualifiers
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/clone="7H12D08"
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Plate: 12 row: D column: 08
Seq primer: -21M13 (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%;
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www.bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                       Email: bbe@tigr.org
Email: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393355.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Pred. No. 0.45;
0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TGGCCAACATGGTGAAACCCGGTCTCTGCTATAAATACAAAAA 103
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Arraying: Greg Lennon, Ph.D.
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Seg primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                 /db_xref="GDB:7621533"
/db_xref="taxon.9606"
/clone="reprint:11-317H22"
/clone="ltb="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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E 1 (bases 1 to 105)

S Hillier L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washb-NCI human EST Project

L Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133644.

Contact: Wilson RK Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRi; Site_2: Not; ist strand cDNA was primed with a Not I - oligo(dT) primer [5'
genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                       AI832832 105 bp mRNA EST 13-JUL-1999 at72q09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377600 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence. AI832832. GI:5454812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Glbco.
Location/Qualifiers
                                                                                                                                                                                                                 9922 TACAAAAATTAGCCGGGCATGGTGGTGCACGCCTGTAATCCCAGCTACTTGGGAGGCTGA 9981
                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                     Score 89; DB 28; Length 105;
                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                        9982 GACAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTACAGTGAGC 10026
                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ixAGE:2377600"
/clone=lib="Barstead colon HPLRB7"
/sex="male"
                                                                                                                                                      Pred. No. 0.61;
                                                                                                                                                                            0; Mismatches
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                                                                                                                                     ch 0.3%;
1 Similarity 90.5%;
95; Conservative (
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Fax: 314 286 1810
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JOURNAL
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KEYWORDS
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Length 105;

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Score 89;

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Query Match

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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pleter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (lifo@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                  20776 AAGCTGAGACAGGAGAATCGCTTGAACCTGGGAGGCGGAGGTTGTGGTGAGCCGAGATCA 20835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                      B48914 103 bp DNA GSS 08-APR-1999 RPCI11-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12, genomic survey sequence.
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       Gaps
                                                                                                  105 AGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGGTTGCGGTGAGGCCAAGATCG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                  20836 TGCCATTGCACTCCAGCCTGGGCAACAAGAGCGAAACTCCGTCTC 20880
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0; Mismatches
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 103
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:7501163"
/db_xref="taxon:9606"
/clone="RPCI-11-4A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
0;
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91.3%;
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B48914.1 GI:2601151
     Conservative
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SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarhini; Hominidae; Homo.

Eutheria; Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 102)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
                                                                                                                                                                              Outbullshed (1998)
Other GSSs: CITBI-E1-2510E2.TF
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madadms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
1 (bases 1 to 109)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: ECORI; Site_2: ECORI;
CalTech Human BAC Library D"
29 c 26 g 30 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9889 GCCAACATGGTGAAACCCTGTCTCTAAAAATACAAAATTAGCCGGGCATGGTGGTG 9948
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    109
    /organism="Homo sapiens"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="2510E2"
/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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88.1%;
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Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
clones are derived from the human BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
RacPac Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@tesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Map Building
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
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                                                                 18-MAY-1999
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 103) 2. Zho.S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 AQ535244 103 bp DNA GSS 18-
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RRPCI-11-317H22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Gaps

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Linher, K.,

/lab\_host="DH10B"

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NOI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.
NOI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.
NOI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.
NOI-GGAP http://www.nobi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
On Jan 19, 1998 this sequence version replaced g1:2151346.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
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Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
/note="Vector: pBeloBACil; Site_1: HindIII; Site_2:
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0; Mismatches 9; Indels 0
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/clone=lib="NCI_CGAP_GG3"
/tissue_type="pooled germ cell tumors"
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
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Search completed: June 14, 2000, 23:50:22 Job time: 40389 sec

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/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                        QY 10905 ATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC 10964
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Pred. No. 0.87;
0; Mismatches 9; Indels 0
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-340-426D-70
US-08-450-673C-70
PCT-US95-17111A-70
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US-08-485-765A-65
US-08-485-765A-65
US-08-481-658B-65
US-08-477-504A-65
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: OS/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
RPPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATPORNEY/AGENT INFORMATION:
US-08-340-426D-70
US-08-450-673C-70
PC-US-08-44-557C-69
US-08-450-653C-69
US-08-450-673C-69
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APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-0021.3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-481-658B-65/c; Sequence 65, Application US/08481658B forter No. 5955075; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                           4004400440004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
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Length 105;

80; DB 4; No. 1.8e-09;

Score (

0.3%;

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US-08-486-756A-65/c
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                                           6147 ATCCCAGCACTTTGGGAGGTCGAGGCAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6206
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  Gaps
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CURRENT APPLICATION DATA:
    APPLICATION DATA:
    APPLICATION NUMBER: US/08/477,504A
    FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
    APPLICATION DATA:
    APPLICATION DATA:
    APPLICATION DATA:
    APPLICATION DATA:
    APPLICATION DATA:
    APPLICATION UNABER: US 08/260,190
    FILING DATE: 15-JUN-1994
    ATTORNEY-AGENT INFORMATION:
    NAME: LAUGHT INFORMATION:
    REGISTRATION NUMBER: 30,863
    REFERENCE/DOCKET NUMBER: D-0021.3D
    TELECHONE: 415-435-2034
    TELECHONE: 415-435-0727
    INFORMATION FOR SEQ 1D NO: 65:
    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.3%; Score 80; DB 4; Length 105;
85.6%; Pred. No. 1.8e-09;
tive 0; Mismatches 15; Indels
0; Mismatches 15; Indels
                                                                                                                                 6207 CIGACCAAAAIGAAGCCIGICICIACIAAAAAIACAAAA 6250
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Sequence 65, Application US/08477504A

Sequence 65, Application US/08477504A

PARENT NO. 5972353

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 6 Maribosa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.6
Matches 89; Conservative
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Matches
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6147 ATCCCAGCACTTTGGGAGGTCGAGGCAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 105;
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Pred. No. 1.8e-09;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: APPLICANT: ANDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: ANDRESSEE: Leona L. Lauder
STREET: ANDRESSEE: ANDRESSEE
ADDRESSEE: Leona L. Lauder
STREET: ANDRESSEE: ANDRESSEE
ADDRESSEE: ANDRESSEE
ADDRESSEE: ANDRESSEE
ANDRESSEE: ANDRESSEE
ANDRESSEE: ANDRESSEE
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ANDRES
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APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-0021.3C
; Sequence 65, Application US/08486756A; Patent No. 5981711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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; Sequence 65, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.3%;
Best Local Similarity 85.6%;
Matches 89; Conservative C
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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US-08-486-756A-65
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RESULT

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TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
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MOLECULE TYPE: DNA (genomic)
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85.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.69
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                  COMPUTER TEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYERM: PC COMPATIBLE
OPERATING SYERM: PC COMPATIBLE
OPERATING SYERM: PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%; Score 80; DB 4; Length 105; ilarity 85.6%; Pred. No. 1.8e-09; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6207 CTGACCAAAATGATGAAACCCTGTCTCTACTAAAAATACAAACA 6250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 CTGGCCAATATGTGAAACCCTGTCTCTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELERAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Application US/08787739 Patent No. 6027887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DX
SOFTWARE: PATENTIN Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            NAME: Lauder, Leona L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
California
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Best Local Similarity
Matches 89; Conserv
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                 USA
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US-08-787-739-65/c
                                       94920
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US-08-485-862B-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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6147 ATCCCAGCACTTTGGGAGGTCGAGGCTGATCACGAGGTCAGGAGTTCAAGACCAGC 6206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 5; Length 105;
Pred. No. 1.8e-09;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6207 CTGACCAAAATGATGAAACCCTGTCTCTACTAAAAATACAAACA 6250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 CIGGCCAATATGGTGAAACCCTGTCTACTACTAAAAA 2
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Sequence 65, Application US/08481658B
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekva, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
STATLE OF INVENTION: MS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAUGHT INFORMATION:
NAME: LAUGHT INFORMATION:
NAME: LAUGHT, LEONA L.
REGISTRATION NUMBER: 30,863
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFRAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-08-477-504A-65
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US-08-486-756A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ITITITACATCTITAGTAGACAGGGTTTCACCATATTGGCCAGGCTGCTCTCAAACTC 60
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGBET INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QY 10951 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CTGACCTTGTGATCCACCAGCCTCCGCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/08477504A Patent No. 5972353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity
Matches 89; Conserv
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US-08-477-504A-65
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US-08-481-658B-65
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QY 10891 TTTTTTGTATTTATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 10950
                                                                                                                                                 1 ITITITACATCITIAGIAGAGACAGGGITICACCAIATIGGCCAGGCIGCTCTCAAACIC 60
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Length 105;
                                                          Indels
                                                                                                                                                                                                                             QY 10951 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION BARE:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                             61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                             16;
Query Match

0.3%; Score 79.4; DB 4;
Best Local Similarity 84.8%; Pred. No. 2.5e-09;
Matches 89; Conservative 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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10891 TTTTTTGTATTTTTATTAGAGATGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTC 10950
                                 1 ITTITAACATCITAACAGAGACAGGGITTCACCATATTGGCCAGGCTGCTCAAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/487,077
                                                                                                          Qy 10951 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10995
                                                                                                                                      61 CTGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-0021.4
                                                                                                                                                                                                                                                                                                ; Sequence 65, Application US/08787739 ; Patent No. 6027887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-981-0332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
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US-08-787-739-65
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                                                                                                                                                          0.3%; Score 79.4; DB 4; Length 105; 84.8%; Pred. No. 2.5e-09; tive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PAPED FLORM:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/477,504
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            QY 10951 CTGACCTCGTGATCCACCCGCTTTGGCCTCCCAAAGTGCTGGGAT 10995
                                                                                                                                                                                                                                                                                                                                                                                                              61 CTGACCTTGTGATCCACCACCTGGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCRMATION:
APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF ENGURCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leander
STREET: 6 Mariposa Court
CITY: Tiburon
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-0021.3D
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Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: ENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                          Query Match
Best Local Similarity 84.89
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.3
Best Local Similarity 84.8
Matches 89; Conservative
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                         HYPOTHETICAL:
ANTI-SENSE:
US-08-486-756A-65
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US-08-485-862B-65
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GENERAL INFORMATION:
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US-08-340-426D-91
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Patent No. 5830670

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CONTY: Mashington
                                                                                                            QY 10891 TTTTTTGTATTTAGAGATGGGGTTTCACCATGTTAGCGAGGATGGTCTCGATCTC 10950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10923 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCCGGTTTGGCCTCCC 10982
                                                                                                                                         1 TITITIACATCITIAGIAGACAGGITICACCATATIGGCCAGGCIGCTCTCAAACIC 60
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                     Length 105;
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0.2%; Score 65.4; DB 3; Length 84;
Best Local Similarity 86.7%; Pred. No. 3.5e-06;
Matches 72; Conservative 0; Mismatches 11; Indels
                                                                   16; Indels
                                                                                                                                                                                                          Qy 10951 CTGACCTCGTGATCCACCCCCTTTGGCCTCCCAAAGTGCTGGGAT 10995
                                                                                                                                                                                                                                   61 CTGACCTTGTGATCCACCACCACGCCTCCCAAAGTGCTGGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                   Score 79.4; DB 5;
Pred. No. 2.5e-09;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
FILING DATE: 30-MAY-1995
FILING DATE: 30-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 0609.3840003
FELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 371-2600
TELEFHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
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; Patent No. 5948634
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                0.3%;
ilarity 84.8%;
Conservative
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LENGTH: 84 base pairs
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                Query Match
Best Local Similarity
Matches 89; Conserv
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US-08-340-426D-91
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10923 CCATGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCACCCGCTTTGGCCTCCC 10982
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                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Ressler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
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Pred. No. 3.5e-06;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0609.3840002
                                                                                                                                                                                                                   COUNTRY: U.S.A.
2IP: 20005-3934
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R.
REGISTRATION UNDBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2500
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPOTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PatentIn Release #1
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Best Local Similarity 86.7%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
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11; Indels

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10923 CCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCCGCTTTGGCCTCCC 10982
                                                                                                                                                                                 0.2%; Score 65.4; DB 6;
86.7%; Pred. No. 3.5e-06;
ative 0; Mismatches 11;
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                                                                  Ouery Match
Best Local Similarity 86.79
Matches 72; Conservative
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STRANDEDNESS: both
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Best Local Similarity
Lag 70; Conserve
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US-08-454-557C-91/c
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PCT-US95-17111A-91
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GENERAL INFORMATION:
APPLICANT: dea la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzhelmer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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Pred. No. 3.5e-06;
0; Mismatches 11; Indels
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21P: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
          APPLICATION UNDER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 3530
ATTORNEY AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LEGTH: 84 base pairs
TYPE: nucleic acid
STRNDEDNESS: both
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Best Local Similarity 86.7
Matches 72; Conservative
CURRENT APPLICATION DATA
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STATE: D.C
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PCT-US95-17111A-91
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US-08-450-673C-91
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Sequence 91, Application US/08454557C
Patent No. 5830670
GENERAL INCRANTION:
GENERAL INCRANTION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Allaheimer's Disease
TITLE OF INVENTION: Of Allaheimer's Disease
TITLE OF ENVENTION: Of Allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
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2IP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAX-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%; Score 62.8; DB 3;
ilarity 85.4%; Pred. No. 1.4e-05;
Conservative 0; Mismatches 12;
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06f
TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 371-2500
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
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Search completed: June 15, 2000 imes 04:56:24 Job time: 57714 sec

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Run on:

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X05251 Human LDL-T
X05251 Human LDL-T
X05249 Human LDL-T
L30244 Human LDL-T
X05248 Human LDL-T
X05248 Human Small
X05208 Human Small
W67808 Human Small
W67808 Human Small
W67809 Human Carci
W67809 Human Carci
M67924 Human Carci
M67924 Human Carci
M67924 Human Small
W57789 Human Seque
X57789 Human Seque
X677804 Human Small
U67806 Human Small
U67807 Human Small
U67807 Human Small
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AR051521 Sequence
K03555 Human Low d
G32906 AD09409 Hum
X91545 H.saplans D
L31299 Human STS U
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U67803 Human small
M87896 Human carci
M87896 Human carci
M87899 Human carci
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G32906 A009W09 Hum
S79560 HRX (intron
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D45223 Human GALNS
M36135 Human alpha
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Human carci
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                                                                                                                                                                                                                                                          X05249 Human
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                                                                                                                                                                                                                                                                                                                                                                                                        HSLDL112
HSU67806
HSU67806
HUMUT8164A
HUMUT8166
HUMUD103M5
HSU67807
HUMLDLRA2
HUMLDLRA2
HUMLDLRA2
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HUMUT8002B
G32906
S79560
HUMD1D03M5
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HSLDLI12
                                                                                                                                                                                                HSLDLRN2
HSLDLRN2
HUMALCE162
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HUMALCE221
HUMALCE221
HUMALCE272
HSLDLRD1
HSLDLRD2
HSLDLRD1
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HSU67808
HSU67808
HUMALCE43
HUMALCE272
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HUMUT931A
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HSU67804
HSBICBR
HSBICBR
HUMLDIRFL
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gb_htg11:*
gb_htg12:*
gb_htg13:*
gb_htg13:*
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      em_htg1:*
em_htg2:*
em_htg3:*
em_hum5:*
                                      gb_p13:*
gb_pr5:*
gb_htg8:*
gb_htg9:*
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Match Length
                                                                                                                                                                                                               81.4
81.4
77.8
77.8
76.2
76.4
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83.8
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71.4
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75.4
75.2
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                                                                                                                                                                        Result
No.
                                                                                                                                                                                                                  June 15, 2000, 04:50:04; Search time 17971.5 Seconds (without alignments) -1569.819 Million cell updates/sec
                                                                                     US-08-852-495C-1_COPY_56000_85000
29001
1 ATGAACAAAGGCTGACTGAT........CAGGAGACTAGAGTTTTATT 29001
                                                                                                                                                               370290
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                               882769 seqs, -486395729 residues
                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Listing first 45 summaries
                                      - nucleic search, using sw model
                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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gb_pl: *
gb_pl: *
gb_pl: *
gb_pr: *
gb_pr: *
gb_pr: *
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gb_htg1:*
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gb_pr4:*
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em_ph: *
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Maximum DB seq length: 110
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Perfect score:
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                                      OM nucleic
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small

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J. Mol. Biol. 271 (2), 222-234 (1997)
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Best Local 9
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HUMALCE162/c
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HSU67803/c
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                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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SOURCE
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                                                                                                                                           Bukaryotta; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarphin; Hominidae; Homo.

1 (Bases I to 108)

1 (Bases I to 108)

1 (Bases I to 108)

Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in the defect in a patient with familial hypercholesterolaemia for Eur.

5 Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saplens
Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutherla;
Eukaryota; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Balislegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia

Eur. J. Blochem. 164 (1), 77-81 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alu repetitive sequence; low density lipoprotein receptor.
                                                                        X05250.1 GI:34337
Alu repetitive sequence; low density lipoprotein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSLDLRN2 108 bp DNA PRI 20-MAY-
Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
                   HSLDLRN2 108 bp DNA PRI 20-MAY
Human LDL-receptor gene intron 14 fragment (normal gene)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.3%; Score 92; DB 10; Length 108; 90.7%; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCAGGAGAATTGCTTGAACCCAGGAGGCAGAGTTGCAGTGAGCCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See X05252 for deletion junction
See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                              See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 108
/note="intron XIV fragment"
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23 c 39 g 18 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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/db_xref="taxon:9606"
1. .108
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                                                                                                                               Homo sapiens
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                                                       X05250
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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                                                                                     24355 CTCGGCTCACTGCAACCTCCGCCTCACGGGTTCAAGCGATTCTCCTGCCTCCGCCTCCCG 24414
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                                                                                                            108 CTGGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCTGGCTCAGCCTCCGG 49
                                                                                                                                                                                                                                                            "" MALCEI62 107 bp ss-RNA PRI 15-APR-1994 Human carcinoma cell-derived Alu RNA transcript, clone CE162. M87924 M87924.1 GI:174871 Alu repeat.
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    Length 108;
                                          10; Indels
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Score 92; DB 10;
Pred. No. 2.1e-06;
0; Mismatches 10
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Human small cytoplasmic Alu transcript.
U67803
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Pred. No. 8e-06;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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30 c 35 g 1
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1 Similarity 91.3%;
94; Conservative
  0.3%;
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Query Match 0.3'
Best Local Similarity 90.7'
Matches 98; Conservative
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MEDLINE AUTHORS JOURNAL

REFERENCE

TITLE

FEATURES

ORIGIN

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QY 24335 CTGGAGTGCTGTGGGCACGTTCTCGGCTCACTGCAACCTCCGCCTCACGGGTTCAAGCGAT 24394
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases; Lo 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu ENA transcripts in human embryonal carcinoma cells. Model opst-transcriptional selection of master sequences
J. Mol. 8101. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. 1992) In press
Location/Qualifiers
                                     HUMAICE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
M87896.1 GI:174874
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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Human carcinoma cell-derived Alu RNA transcript,
M87899
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Pred. No. 5.3e-05;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83.6; DB 9;
Pred. No. 5.8e-05;
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90.8%; Pred. No. 5.8e-v
.... 0; Mismatches
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26 c 37 q 1
                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/cell_line="NTera2D1"
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27 c 33 g 1
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/sex="male"
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Best Local Similarity 88.3
Matches 91; Conservative
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2 (bases 1 to 108)
Shalkh, TH., Kim, Datzer, M.A. and Deininger, P.L.
Direct Submission
Submitted (22-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     11616 GTAGATACGGGGTTTCACTTTGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCG 11675
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               Length 108;
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Pred. No. 4.9e-05;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
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                                                                                                                                                                                                                                                                                                                                                             DB 11;
1e-05;
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Pred. No. 1e-05
0; Mismatches
                                                                                                                                                                                                                                                                                    16
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                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
1. .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="carcinoma"
27 c 33 g 1
                                                                                                                                                                                                                                               /rpt_family="Alu"
/rpt_type=dispersed
39 c 30 g
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/sex="male"
                                                                                                                                                                                                                               /note="scAlu"
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Best Local Similarity 90.0'
Matches 90; Conservative
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Best Local Similarity 94.89
Matches 91; Conservative
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Williamson, R. and Humphries, S.
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1 (Abases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Brr. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See X05248 for corresponding normal gene sequence. In the defective LDL-receptor gene the deletion courred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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1. .108
//note="deletion junction region intron 12/ intron 15"
40 c 20 g 28 t
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251.1 GI:34336
                                                                                                                                                                                                                            20-MAY-1992 deletion junction.
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                 17799 CCATGTIGGICAGGCIGGICITAAACICCIGACCICAIGAICIGCCCACCICAGCCICCI 17858
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Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 108)
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                                                  104 ccargriagccaggcregrerreaacrecregecregearcrecerecregecreec
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Alu repetitive sequence; low density lipoprotein receptor
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Pred. No. 7.3e-05;
0; Mismatches 15; Indels
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                                                                                                                                                                                                          HSLDLRD1 108 bp DNA PRI
Human LDL-receptor mutated gene with intron 12
X05249
                                                                                                             AAAGTGCTGGGATTACAGGAGTGAGCCACCGCGCCCGGCCAGA 2
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/db_xref="taxon:9606"
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Best Local Similarity 86.0%;
Matches 92; Conservative C
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VERSION
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SOURCE
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*Source: hypercholesterol aemia
See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
allu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (0'-DEC-1987) by HUMPHRIES S.
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See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
Eur. J. Blochem. 164 (1), 77-81 (1987)
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Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
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Pred. No. 7.3e-05;
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Best Local Similarity
Matches 92; Conservat
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarniai; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Basisgel, U., Dunning, A., Havinga, J.R., Milliamson, R. and Humphries, S. Unequai crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
density lipoprotein.
                                                                                                                                                                                 Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome sequence tagged sites from the human genome Unpublished (1994)

Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics Salt Lake City, UT 84112

Salt Lake City, UT 84122

Finer A: AGAGGTTGCAGTGAACCAA

Primer A: AGAGGTTGCAGTGAACCAA

Primer A: AGAGGTTGCAGTGAACCAA

Brimer B: TTTTCCCCTCTACTACTA

End to Label: Frimer B

PCR Profile:
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 91) Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4131 TCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACATTGCACTCCAGCCTGGGTGACA 4190
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Alu repetitive sequence; low density lipoprotein receptor;
repetitive sequence.
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91.2%; Pred. No. 0.00049;
tive 0; Mismatches 8; Indels
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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    .91
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/evidence-experimental
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See X0520 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion aliminates axons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)

1 (bases 1 to 108)

1 (bases 1. to 108)

Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. 3. Blochem. 164 (1), 77-81 (1987)
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STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; tetranucleotide repeat.
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Human STS UT8164, 5' primer bind, sequence tagged site.
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                      Length 108;
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                    0.3%; Score 81.4; DB 10;
85.0%; Pred. No. 0.00014;
iive 0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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1 (bases 1 to 108)
Shakkh, T. H., Roy, A. M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAS derived from primary and small cytoplasmic Alu (scAlu)
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Pred. No. 0.00045;
0; Mismatches 16; Indels 0
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Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Direct Submission
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Human small cytoplasmic Alu transcript.
UG7803.
UG7803.1 GI:2289917
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g 29 t
                             /organism="Homo saplens"
/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"

    108
    /organism="Homo sapiens"
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/note="intron XII f;
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1. .108
/note="scAlu"
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88; Conservative
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model opost-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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HUMALCE43 110 bp ss-RNA PRI 15-APR-199
Human carcinoma cell-derived Alu RNA transcript, clone CE43.
M87900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.3%; Score 77.8; DB 9; Length 110; llarity 83.8%; Pred. No. 0.00057; Conservative 0; Mismatches 17; Indels
                                                                                                         Alu repeat.
Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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31 c 34 g 16
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Best Local Similarity
Matches 88; Conserv
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T24892
ID T24892 standard; CDNA to mRNA; 100 BP.
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00000000000
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                Query Match
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                                                                             1 ATGAACAAAGGCTGACTGAT......CAGGAGACTAGAGTTTTATT 29001
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                      hits satisfying chosen parameters:
                                                                 US-08-852-495C-1_COPY_56000_85000
                                                                                                           311585 segs, 125096042 residues
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Listing first 45 summaries
                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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X12087
X12085
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T22572
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Match Length D
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Maximum DB seq length: 110
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS sequences couple-stranded DNA) which comprises one of the 7837 "GS sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end in the particular mRNAs in the pacticular with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                Simple tandem repe
Human gene signatu
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05-NOV-1996 (first entry)
Gene signature HUMGS06998.
Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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ID T24892 standard; cDNA to mRNA; 100
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11-NOV-1994; J01916, 
12-NOV-1993; JP-355504, 
(MATS/) MATSUBARA K. 
(OKUB/) OKUBO K.
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Claim 1; Page 2182; 2245pp; Japanese.
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Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4120 ATCACTTAAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCATTGCACTCCAG 4179
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                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                             WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 0.019;
0; Mismatches
                                                                                    cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126828 standard; cDNA to mRNA; 108
                                 Human gene signature HUMGS06998.
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14-NOV-1996 (first entry)
Human gene signature HUMGS09078.
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80.8%;
                  (first entry)
                                                                                                                                        01-JUN-1995.
11-NOV-1994; JO1916.
12-NOV-1993; JP-355504.
(MAT'S.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-00V-1994; J01916.
12-NOV-1993; JP-35564.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
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                                                                                                                                                                                                                                  Okubo K;
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Best Local Similarity
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                                                                                                       Homo sapiens.
WO9514772-A1.
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                  05-NOV-1996
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T26828/c
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While you soldated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity resting or phenotypic typing for disease

Election 1: Page 219; 310pp; English.

Claim 1: Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Eabry's disease, familial hypercholasterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary camorrhagic telangtectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microcorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, conturance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid copyplaxis of such diseases.
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double-stranded DNA, which complementary strand or the corresp.

double-stranded DNA, which comprises one of the 7837 "GS" sequences
given in 119001-126837 and which is able to hybridise to part of
thuman genomic DNA, cDNA or mNAM is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mNAM by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mNAM species, almost
all the 3'-oriented cDNAs hybridise with specific mNAMs. Each library
is constructed so as to reflect accurately the relative abundance of
different mNAMs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
sequence 108 BP; 18 A; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24971 ACAATTAAAAAAAAAAAAAAAGGCTGGGCGGGGGGCTCACGCCTATAATCCCAGCTCTTT 25030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human biallelic polymorphic DNA fragment TIGR-A003M18a. Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%; Score 68.8; DB 1; Length 108; 80.6%; Pred. No. 0.032;
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0; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X12095 standard; DNA; 108 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 80.6
Matches 79; Conservative
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06-NOV-1996; US-030455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9820165-A2.
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Query Match Best Local &

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4120 ATCACTTAAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCATTGCACTCCAG 4179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from marious human tissues; synthesis of cDNA mas initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Beah library is constructed so as to reflect accurately the relative abundance of different mRNAs, in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ATCACTTGAGCCTAGGAGGCAGNGGTTCAAGTGAGCTGAGATGGCACTCCTGCGCTCCAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsubara K, Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                     Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                  WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 0.15;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1944; 2245pp; Japanese.
                                             T25854 standard; cDNA to mRNA; 91 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T26828 standard; cDNA to mRNA; 108
                                                                                     22-OCT-1996 (first entry)
Human gene signature HUMGS08084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene signature HUMGS09078.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSCHARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.2
Best Local Similarity 80.9
Matches 72; Conservative
                                                                                                                                                                                                                                                  01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                  Okubo K;
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WO9514772-A1.
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                                                                  T25854;
22-0CT-1996
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  RESULT
T25854
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Hudson T, Lander ES, Wang D;

WPI: 98-286974/25.

Presided unucleic acid segments from the human genome - used for mew isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease

Preside and the sease occupying the polymorphic site is indicated by commerces which have been isolated using the primers represented in commerces which have been isolated using the primers represented in comparing the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in comparing to a grammagical polymorphic forms in an individual for use in comparing the seases in the seases of such as agammagical individual colonic polyposis, Elers-Danios spacetonesis in polycystic kidney disease, hereditary comparing special inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such contrance diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such contrance, fertility, and susceptibility or receptivity to particular culuar contrance, can be used to produce medicaments for the treatment or contrance of such assessed to produce medicaments for the treatment or contrance.
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                                                                                                                                                        7604 CIGTAAICCCAGCAC-TITGGGAGGCTGAGGIGGAIGGAICACCTGAGGIIGGGAGIIIG 7662
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment TIGR-A003M18a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autofumune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                               Gaps
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Pred. No. 0.12;
1; Mismatches 18; Indels
                                                                    Length 108;
                                                                                                                                                                                                                                                7663 AGACCAGCCTGGCCAACATGGTAAAACCCCATGTCTACTAAAAATACA 7710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY 19612 CAGGCGATCTGCCCGCCTCCAAA-GTGCTAGGATTACAG 19656
                                                                                                             18; Indels
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                                                                Score 66.8; DB 1
Pred. No. 0.063;
1; Mismatches 1
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28
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23
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Sequence 108 BP; 19 A;
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                                                                                                             88; Conservative
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06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST E
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Best Local Similarity
                                                                                       Similarity
BP;
108
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63

Matches

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17; Indels

18 T;

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33 A;

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RESULT
T20927
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                                                                      A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in Ti9001-T26837 and which is able to hybridise to part of ni Ti9001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA hibraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-en of mRNA by using poly(T) as the sole primer. Since the 3'-en untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library call form the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequence) as a means of diagnosing abnormal cell function or for recognising different cell types. 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared communant values human tissues; synthesis of CDNA was initiated from the CS 3'-end of mRNA by using poly!(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNN; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%; Score 64.4; DB 1; Length 108; 80.4%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GAGCCACCACGCCCGGCTGTTTTATTTCTTAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T26213 standard; cDNA to mRNA; 103 BP
                                                          Page 2182; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2029; 2245pp; Japanese.
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Human gene signature HUMGS08452.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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                                                              Claim 1;
                                          tissues
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                                                                                                                         10154 GATCTCTTGAGCCTAGAAGTTTGGGGACGCAGTGAGCTATGATTATGCCACTGCACTCCA 10213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA libraries prepared from various human tissues; synthesis of cDNA intracted from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented conNa hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
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                                                                                                                                                           1 GATCACTTGAGTCCAGGAGTTGGTGTTACAGTGAGCTATGATGGTGCACTCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120927;
24-JuL-1996 (first entry)
24-JuL-1996 (first entry)
Human gene signature HUMGS02180.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
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         Length 103;
                                                                 Indels
                                                                                                                                                                                                                                         Qy 10214 GCCTGGGCAACAATGCAAAATCCTGTCTCAAAAACAAAACA 10255
                                                                                                                                                                                                                                                                            Qy 17764 CTAATTTTTGTATTTTTAGAAGAGACGGAATTTCACCATG 17803
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   Score 63.6; DB Pred. No. 0.19; 0; Mismatches
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ID T20927 standard; cDNA to mRNA; 103 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          T20927 standard; cDNA to mRNA; 103
   0.2%;
Query Match 0.29
Best Local Similarity 76.5
Matches 78; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okubo K;
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Query Match
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Claim 1: Page 758-759; 2245pp: Japanese.

Claim 1: Page 758-759; 224pp: Japanese.

Claim 1: Page 758-759; 227 pp: Japanese.

Claim 1: Page 758-759; 227 pp: Japanese.

Claim 2: Page 758-759; 227 pp: Japanese.

Claim 2: Page 758-759; 27 pp: Japanese.

Claim 3: Page 758-759; 27 pp: Japanese.

Claim 4: Page 758-759; 27 pp: Japanese.

Claim 4: Page 758-759; 27 pp: Japanese.

Claim 4: Page 758-759; 27 pp: Japanese.

Claim 5: Page 758-759; 27 pp: Japanese.

Claim 6: Page 758-759; 27 pp: Japanese.

Claim 7: Page 758-7
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22-OCT-1996 (first entry)
Human gene signature HUMGS08084.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
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Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                Human gene signature HUMG502180.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
WO9514772-A1.
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Homo sapiens.
WO9514772-Al.
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                                          24-JUL-1996 (first entry)
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Best Local Similarity 76.5
Matches 75; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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(OKUB/) OKUBO K.
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WPI; 95-206931/27.
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T25854/c
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Claim 1; Page 1944; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences: given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 91 BP; 18 A; 22 C; 28 G; 18 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17618 TGAAATAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGGCGCAATCTCAGCTCACT 17677
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences quiven in 719001-726837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 TGAGACASNNTCTCACGCTGTCACCNAGGCTGGAGCGCAGGAGTGCCATCTCAGCTCACT 31
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Human gene signature HUMGSOB452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
HOMO Sapiens.
W09514772-A1.
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25 G; 23 T;
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78.78;
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Matches 70; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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us-08-852-495c-1\_copy\_56000\_85000.rng

Local

Matches

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determining polymorphic forms for use in e.g. forensics, paternity determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease

Zidaim 1: Page 218; 310pp; English.

Xi0569-Xi2937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in markers which have been isolated using the primers represented in consists which have been isolated using the primers represented in markers which have been isolated using the primers represented in consists which have been isolated using the primers represented in markers which have been isolated using the primers can be used in methods for determining polymorphic forms in an individual for use in conscious paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial colonic polyposis, Ehlers-Danios syndrome, osteogenesis inperfected, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous syndrome, osteogenesis is imperfected, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous syndrome, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic or decided of the content or as longer to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4913 TGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCATCTGAGG 4972
                           30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276c.
Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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Polymorphism, biallelic; human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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                                                                                                                                                                                                                                                                                                                                                                                        Hudson T, Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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05-NOV-1997.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
Hudson T, Lander ES, Wang D;
WPPI: 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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0.71:
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1; Mismatches
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AC X12086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment EST98276a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typhing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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74.0%; Pred. No. 0.71;
Ive 1; Mismatches 25; Indels
   DB 1; Length 103;
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                               Pred. No. 0.44;
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0.2%; Score 61; 75.2%; Pred. No. (
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X12085 standard; DNA; 100 BP

RESULT 14

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PT determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
PS Claim 1. Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic x10269-X12937 are human DNA fragments which contain biallelic polymorphic commarkers which have been isolated using the primers represented in committees which have been isolated using the primers represented in committees appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in commence. The as agammagalobulinmenta, diabetes institutes, Lesch'Nyhan syndrome, cauch as agammagalobulinmenta, diabetes institutes, Fesch'Nyhan syndrome, muscular dystrophy, Wiskott-Aidrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microcytanisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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4913 TGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCATCTGAGG 4972 100 TGTGACTCACCACCTATAATCCTGGCACTTTAGGAGGCTKAGGAAGGAGGATGTTTGAAA 41 4973 TCAGAAGTTCCAGACCAGCCTGGCCAACATGGCGAAACCC 5012 ð ò 윱

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Ouery Match 0.2%; Score 59.6; DB 1; Length 100; Best Local Similarity 74.0%; Pred. No. 0.71; Matches 74; Conservative 1; Mismatches 25; Indels

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Copyright (c) 1993 - 2000 Compugen Ltd.
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AQ003188 RPCI11-13
AQ36882 RPCI11-13
AQ264176 CITBI-EI-AA44245 nc07a04.s
H67040 yu68c01.r1
AA812141 ob48h02.s
AA897366 am06h02.s
AA56553 RA42b11.s
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B17434 345K2 TVB C
AIO77628 0926f04.s
AA835205 ak64h01.s
B48914 RPCIII-4A12
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AQ386882 RPCI11-13
                                                                                                                                                                                                                                                                                                                                                                                AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNr neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
             AA703692 ag81a10.r
AA243009 zr25h02.s
                                                                                                                                                              AQ028649 CIT-HSP-2
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1 (bases 1 to 106)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Ladoy,M., Le,N., Lennon,G., Marrata,M., Marthn,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Materston,R. and Wilson,R. WashC. Nori human EST Project
Unpublished (1997)

On Sep 12, 1996 this sequence version replaced g1:1397630.
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/dev_stage="hNT neurons"
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/note "vector: pBluescript SK; Site_1: BcoRI; Site_2:
/note "vector: pBluescript SK; Site_1: Ste_1: SkoI; cloned unidirectionally. Primer: Oligo dT.
/note="vector: pBluescript" SK; Site_1: Ste_2: Ste_2: SkoI; Site_2: Ste_2: SkoI; Site_2: Ste_2: SkoI; Site_3: Ste_2: SkoI; Site_3: Ste_2: SkoI; Site_3: SkoI; 
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Drimates; Catarrhini; Hominidae; Homo.

Eutheria; L. Allae, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marrin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project

Unpublished (1997)

On Dec 3, 1996 this sequence version replaced gi:1126869.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810

Email: est@watson.wustl.edu
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IRAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3 revi ET from Amersham
High quality sequence stop: 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1127 Std Error: 0.00
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Pred. No. 0.044;
0; Mismatches 7; Indels
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High quality sequence stop: 102.
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Gaps

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Eukaryotating Saptating Statements (Lases) Eukaryotating Saptating Saptating Saptating Saptating Statements (Lases) Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 100)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Tumor Gene Index

Connact: Robert Strausberg, Ph.D.

Connact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@enih.gov

This clone is available royalty-free through Lint.; contact the IMAGE Consortium (info@image.lini.gov) for further information.

Trace considered overall poor quality
Insert Length: 820 Std Error: 0.00

Seq primer: -40ml3 fwd. Er from Amersham

High quality sequence stop: 1.

Location/Qualifiers
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/clone_lib="Soares_senescent_fibroblasts_NbHSF"
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/itssue_type="senescent_fibroblast"
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/note="Vector: pr7730 (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
primer [5'
primer [5'
retraccantcrdaagregeagegegeccecantryrryrryrryrryrryryryryryryryry])].
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                                                                                                                                                                                                                              19558 TAGTAGAGATGGGGTTTCACCATGCTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGCG 19617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oy26f04.sl Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1666975 3' similar to qb:x57130_cds1 HISTONE H1D (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                               109 TAGTIGAGACGGGGTITCACCATGGTGGCCAGGCTGGTCGTCGGAACTCCCGACCTCAGGTG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1998
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                                                                                                   Length 109;
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93.0%; Pred. No. 0.22;
tive 0; Mismatches 7;
                                                                                                   Score 91.4; DB 84;
Pred. No. 0.11;
                                                                                                                                                                  0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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AI077628.1 GI:3412036
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Best Local Similarity
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                                                                                                                             Local Similarity
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AI077628/c
LOCUS
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KEYWORDS
SOURCE
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E (bases 1 to 109)

S Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building
L Unpublished (1997)

Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Teal: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are available from Research Genetics (info@resgen.com). BAC
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/cell_type="fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library Al"
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345K2.TVB CIT978SKAl Homo sapiens genomic clone A-345K02, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.4; DB 30;
Pred. No. 0.11;
0; Mismatches 11;
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
Location/Qualifiers
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Best Local Similarity 89.9%;
Matches 98; Conservative
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Class: BAC ends.
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Gaps

ORGANISM

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SOURCE

VERSION

REFERENCE AUTHORS

ACCESSION

AA835205

RESULT

g δ g TITLE JOURNAL

COMMENT

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Email: Judadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong mac.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Ettheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
1 (bases 1 to 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B17434 109 bp DNA GSS 04-JUN-1998
345K2.TVB CIT978SKAl Homo sapiens genomic clone A-345K02, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBAC63.6; Site_1: EcoR1; Site_2: EcoR1; RPC111 Human Male BAC Library"
28 c 30 g 15 t
                           B48914 103 bp DNA GSS 08-APR-1999 RPCI11-4A12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-4A12, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 109)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 103;
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Pred. No. 0.23;
0; Mismatches
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/note="Yector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:7501163"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RPCI-11-4A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11"
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Best Local Similarity 91.3%;
Matches 94; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
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                                                                                                                                                                   B48914.1 GI:2601151
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848914/c
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B17434
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 101)
S Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Waylie,T., Waterston,R. and Wilson,R.
Unpublished (1997)
Con Nov 29, 1993 this sequence version replaced gi:636191.
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                 AA835205 101 bp mRNA EST 23-FEB-1998 ak64h01.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412689 3' similar to contains Alu repetitive element; contains element KER repetitive element ;, mRNA sequence. AA835205
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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100 AAGAGCCTGTGGAGCAAGGCGACTCTAGTGCAAACGAAAGGCACCGGTGCTTCTGGCTCC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1412689"
/clone_lib="Barstead pancreas HPLRB1"
                                                              QY 11513 CAAGCTCCGCCTCCCGGATTCACGCCATTCTCCTGCCTCA 11552
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Pred. No. 0.22;
0; Mismatches
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/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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il Similarity 93.0%;
93; Conservative
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FEATURES

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Indels

Matches

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RESULT

Gaps

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13; Indels

Length 109;

53

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 110)

S Adams, M.D.; Rounsley, S.D.; Zhao, S.,; Fleld, C.E.; Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Upoublished (1998)

L Unpublished (1998)

L Ontact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: maddams@tipr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lnfo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                             ON 17610 TITITITITITAAAATAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGGCGCAATCTC 17669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ003188 110 bp DNA GSS 14-APR-1999 RPCI11-1D10.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1D10, genomic survey sequence.
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1_Human Male_BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1313G15"
/sex="Male" cIT-HSP"
/sex="Male" Sperm"
/cell_Lyppe="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
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Pred. No. 0.25;
0; Mismatches 13;
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/db_xref="GDB:7500081"
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/clone="RPCI-11-1D10"
/clone_lib="RPCI-11"
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Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building
L Onpublished (1997)
Other GSSs: 345K02.TP 345K02.TPB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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1 (bases 1 to 109)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
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/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
Calrech Human BAC Library A1"
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
721: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
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11arity 88.1%; Pred. No. 0.25;
Conservative 0; Mismatches 13; Indels 0;
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/db_xref="taxon:9606"
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/clone_lib="CIT978SKA1"
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Other_GSSS: RPCIII-134I4.TJ

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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
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RPCI11-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
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1 (bases 1 to 110)

2 hao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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Pred. No. 0.25;
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/db_xref="GDB:7551267"
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/clone="RPCI-11-13414"
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Homo sapiens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
class: BAC ends.
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t
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                                                                                                                                               AQ264176 106 bp DNA GSS 27-OCT-1998 CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2, genomic survey sequence.
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Pred. No. 0.37;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy 11685 AGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGCCACTGCGCCCGG 11730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
Other GSSs: CITBI-E1-2509A2.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 and 838 0200
Fax: 301 838 0208
46 GGTCTCCCAAAGTGCTGGGATTACAGGCGTGAGACTCTGCGCCCGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male
/cell_type="sperm"
/note="Vector: pBeloBAC11;
Calrech Human BAC Library C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .106
/organism="Homo sapiens"
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human.
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KEYWORDS
SOURCE
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ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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l (bases 1 to 107).

thilser.L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, M., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Mortis, M., Parsons, J., Prange, C., Rifkin, L.,
Rohliing, T., Schellenberg, K., Soares, M.B., Tan, F., Thlerry Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10997 TAGCTGGGCGTGGTGGCACATGCCTGTAGTCCCAGCTACTGGGGAGGCTGAGGCAGGAGA 11056
                                                                                                                                                                                            Generation and analysis of 280,000 human expressed sequence tags Genera Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
High quality sequence stops: 101
Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 TAGCTGGGTGGTAGCACATGCCTGTATTCCNAGCTACTCAGNAGGCTGAGGTAGGAGAA 48

        B65160
        108 bp
        DNA
        GSS
        21-JUN-1998

        CIT-HSP-2017G2.TRB CIT-HSP Homo saplens genomic clone 2017G2, genomic survey sequence.
        865160.
        865160.
        GI:2639138

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthería; Primates; Catarrhini; Hominidae; Homo.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
                                                                                                                                                                                                                                                       97044478
On Nov 29, 1993 this sequence version replaced gi:429999.
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .107
/organism="Homo sapiens"
/db_xref="GDB:3864328"
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/clone=lib="Weizmann Olfactory Epithelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy 11057 ATTGCTTGAACTCGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGC 11103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 others
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.3%;
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                                                                                                                                                                                 and Marra, M.
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Best Local Similarity
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ORIGIN
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COMMENT
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B65160/c
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  REFERENCE
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KEYWORDS
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                        AUTHORS
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                                                                                                                                                                                                       TITLE
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                                                                                                                                              Tumor Gene Index

Unpublished (1997)
On Jan 24, 1995 this sequence version replaced gi:634306.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergehingov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consorttum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="45 years old"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAWP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman." I others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY 17609 TTTTTTTTTTGAAATAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGCGCAATCT 17668
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 110) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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86.4%; Pred. No. 0.38;
iive 0; Mismatches 15; Indels 0
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High quality sequence stop: 90.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-"IMAGE:1007406"
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H67040.1 GI:1025780
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Best Local Similarity 86.4%
"...hes 95; Conservative
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BASE COUNT ORIGIN

source

FEATURES

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Gaps

RESULT 13 H67040/c LOCUS

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DEFINITION

ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

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                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Ml3 Reverse
Class: BAC ends.
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Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27881 TGGGCAGTGGCGTGATCTCGGCTCGCTGCACCTCCCGGGTTCAAGTGATTCTC 27940
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 106)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1402063.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85.8; DB 84; Length 108;
Pred. No. 0.48;
0; Mismatches 12; Indels 0
                                                                                       Unpublished (1997)
Other_GSSs: CIT-HSP-2017G2.TFB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 938 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QY 27941 CTGCCTCAGCCTCCTTAGTAGCTGGGACCACAGGCGCATGCCATC 27985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 88.6%;
Matches 93; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
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                                                                    Building
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AUTHORS
TITLE
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/clone_lib="NCI_CGAP_GCB1"
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/lab_host="DH10B"
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High quality sequence stop: 60.
Location/Qualifiers
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                          /organism="Homo sapiens"/db_xref="taxon:9606"
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Best Local Similarity 87.7'
Matches 93; Conservative
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
US-08-450-673C-92
PCT-US95-17111A-92
PCT-US95-17111A-92
US-08-454-557C-60
US-08-454-657C-60
US-08-454-557C-60
US-08-454-557C-69
US-08-454-557C-69
US-08-454-557C-69
US-08-486-656-66
US-08-486-556A-66
US-08-486-556A-66
US-08-485-862B-66
US-08-485-865B-66
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Pred. No. 1.3e-09;
                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/481,658B FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA: US 08/260,190 FILING DATE: 15-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-0021.3E
                                                                                                                                                                                                                                                                                            65, Application US/08481658B
3, 5955075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/FOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                       Leona L. Lauder
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LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: USA
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Sequence 65, Application
Patent No. 5955075;
GENERAL INFORMATION:
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US-08-481-658B-65
  RESULT
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/cgn2_6/ptodata/1/ina/R_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-486-756A-65
US-08-486-862B-65
US-08-481-658B-65
US-08-481-658B-65
US-08-486-756A-65
US-08-486-756A-65
US-08-787-739-65
US-08-787-739-65
US-08-340-4260-91
US-08-450-673C-91
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US-08-340-426D-92
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Listing first 45 summaries
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                                                                                June 15, 2000, 04:56:24
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Maximum DB seq length: 110
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0; Mismatches 13; Indels
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SOFTWARE PATENTIN Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/477,504A
FILING DATE OF JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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Pred. No. 1.3e-09;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                            APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
ATTLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94920
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               Sequence 65, Application US/08477504A Patent No. 5972353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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87.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
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91; Conservative
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Best Local Similarity
Matches 91; Conserva
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US-08-477-504A-65
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27998 TTTTTGTATTTTATTAGAGACAGGGTTTCACTATGTTGGCCAGGCTGATCTCAAACTCC 28057
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Pred. No. 1.3e-09;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY, AGENT INFORMATION:
NAME: LAUGET, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Fatent No. 5989838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                  APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
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Sequence 65, Application US/08486756A
Patent No. 5981711
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.3%;
Best Local Similarity 87.5%;
Matches 91; Conservative (
                                                                                                                                                                                                                                6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. I
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   STREET: 6 Mariposa
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   잁
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                ZIP: 94920
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US-08-486-756A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-485-862B-65
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RESULT

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nucleic acid
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORMUTER: IBM PC compatible
CORMUTER: IBM PC compatible
CORMUTER: Parentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Parentin Release #1.0, Version #1.30 (EPO)
CURSIFICATION NUMBER: US/08/485,862B
FILING DATE: 07-UUN-1995
CLASSIFICATION NUMBER: US 08/477,504
FILING DATE: 07-UN-1995
ATTORNEY/AGENT NUMBER: US 08/477,504
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3D
FLEEPHONE A15-435-4073
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
California
                   USA
                                    94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-485-862B-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-787-739-65
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27998 ITTTTGTATTTTATTAGAGACAGGGTTTCACTATGTTGGCCAGGCTGATCTCAAACTCC 28057
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Pred. No. 1.3e-09;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 28058 TGACCTCA.TGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGAT 28101
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Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Bastorekowa, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INFORTION: MN Gene and Protein
WUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/47,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
ATTORNEY APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/POCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.39
Best Local Similarity 87.59
Matches 91; Conservative
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linear
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US-08-477-504A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 4; Length 105; 3e-09;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3E
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
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APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 4.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25078 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAAGTATAAAAA 25121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 CTGGCCAATATGGTGAAACCCTGTCTACTACTAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.3%; Score 81.6; D
Best Local Similarity 86.5%; Pred. No. 3e-0
Matches 90; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-504A-65/c
; Sequence 65, Application US/08477504A
; Patent No. 5972353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
F: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11ne
MOLECULE TYPE: I
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
US-08-481-658B-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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25018 ATCCCAGCTCTTTGGGAGGCCTAGGCGGGTGGATCACGAGGTCAGGAGTTCAAGACCAGC 25077
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                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                               DB 4; Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY 25078 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAGTATAAAAA 25121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 CTGGCCAATATGGTGAAACCCTGTCTACTACAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-084 866756A-65/C

Sequence 65, Application US/08486756A

Sequence 65, Application US/08486756A

Sequence 65, Application US/08486756A

Setent No. 5991111

SEPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorekova, Jaromir

TITLE OF INVENTION: M Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 6 Mariposa Court

CITY: Tiburon

STATE: California
                                       D-0021.3D
NAME: Lauder, Leona L.
REGIETRATION UNDHBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                  LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Page

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25018 ATCCCA3CTCTTTGGGAGCCTAGGCGGGTGGATCACGAGGTCAGGAGTTCAAGACCAGC 25077
                           OPERATING SYSTEM: PC-DOSC/MS-DOS
OOFWARTE: Petentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
APPLICATION NUMBER: US 08/485,049
FILING DATE: O7-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: O7-JUN-1995
PRIOR APPLICATION NUMBER: US 08/487,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: LAUGHT. LEGNATION:
NUMBER: LAUGHT. LEGNATION:
NUMBER: LAUGHT. LEGNATION:
NUMBER: LAUGHT. LEGNATION NUMBER: 30,863
                                                                                          Qy 25078 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAGTATAAAAA 25121
                                                                                                                        45 CIGGCCAATATGGTGAAACCCTGTCTACTACTAAAAA 2
                                                                                                                                                                                                                                                        Sequence 65, Application US/0878739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYFE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: D. TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 105 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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STRANDEDNESS:
                                                                                                                                                                                                                  RESULT 10
US-08-787-739-65/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
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US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                         25018 ATCCCAGCTCTTTGGGAGGCCTAGGGGGGTGGATCACGAGGTCAGGAGTTCAAGACCAGC 25077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                          Query Match 0.3%; Score 81.6; DB 4; Length 105; Best Local Similarity 86.5%; Pred. No. 3e-09; Matches 90; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81.6; DB 4; Length 105;
Pred. No. 3e-09;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94920

ZIP: 94920

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                      25078 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAGTATAAAAA 25121
                                                                                                                                                                                                                                                                                                                                                               45 CTGGCCAATATGGTGAAACCCTGTCTTATAAAGATGTAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-485-862B-65/C
Sequence 65, Application US/08485862B
Fatent No. 5989838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-070-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECHOME: 415-435-2034
TELECHOME: 415-435-2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-0021.3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%;
Best Local Similarity 86.5%;
Matches 90; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                          ; ANTI-SENSE: NO
US-08-486-756A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-08-485-862B-65
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GENERAL INFORMATION
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US-08-340-426D-91
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US-08-450-673C-91
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: della Monte, Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: A Albeimer's Disease
NUMBER OF SEQUENCES: 121
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11636 TGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGGCCCGCCTCAGCCTCCCAAA 11695
                                                                                                           25018 ATCCCAGCTCTTTGGGAGGCCTAGGCGGGTGGATCACGAGGTCAGGAGTTCAAGACCAGC 25077
                                                                                                                                     105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACAAGGTCAGGAGTTTGAGAGCAGC 46
                                                                    Gaps
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                    0.3%; Score 81.6; DB 5; Length 105;
86.5%; Pred. No. 3e-09;
tive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%; Score 67.2; DB 3; Length 84; 90.0%; Pred. No. 3.8e-06; cive 0; Mismatches 8; Indels
                                                                                                                                                                                                Qy 25078 CTCGCCAAGATGGTGAAATCCCGTCTCTACTAAAAGTATAAAAA 25121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: U.S.A.

ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILLING DATE: 30-MA-1995
CLASSIFICATION: 514
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                            45 CTGGCCAATATGGTGAAACCCTGTCTCTACTAAAGATGTAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 91, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                   Sequence 91, Application US/08454557C Patent No. 5830670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY 11696 GTGCTGGGATTACAGGAGTG 11715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 GTGCTGGGATTACAAGCGTG
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Best Local Similarity 90.0
Matches 72; Conservative
                                           Best Local Similarity 86.5
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Wash
STATE: D.C
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US-08-340-426D-91
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                    Query Match
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Sequence 91, Application US/08450673C
Patent No. 594888
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Of Allaheimer's Disease
TITLE OF INVENTION: Of Allaheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: A lalbeimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11636 TGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGGCCCGCCTCAGCCTCCCAAA 11695
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                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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Pred. No. 3.8e-06;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISCHARTION UNBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0609.3840002
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palana
                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 11696 GTGCTGGGATTACAGGAGTG 11715
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Best Local Similarity 90.0%;
Matches 72; Conservative
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8; Indels

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Qy 11636 TGTTAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCGGCCCGCCTCAGCCTCCAAA 11695
                                                                                                                                       0.2%; Score 67.2; DB 6;
90.0%; Pred. No. 3.8e-06;
ative 0; Mismatches 8
                                                                                                                                                                               Qy 11696 GTGCTGGGATTACAGGAGTG 11715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CGACACCAGCCTGATGAACATGG 1
                                                                                                                                                                                               64 GTGCTGGGATTACAAGCGTG 83
                                                           Query Match 0.29
Best Local Similarity 90.09
Matches 72; Conservative
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20005-3934
               PCT-US95-17111A-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-454-557C-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                 0.2%; Score 67.2; DB 4; Length 84;
90.0%; Pred. No. 3.8e-06;
Live 0; Mismatches 8; Indels
                    PILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lidwig, Steven R.
REGISTRATION NUMBER: 36,203
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ludwig, Steven R.
REGISTRATION UNBABER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
              APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                       Qy 11696 GTGCTGGGATTACAGGAGTG 11715
                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GTGCTGGGATTACAAGCGTG 83
                                                                                                                                                                                                                                                                                               Query Match 0.2%
Best Local Similarity 90.0%
Matches 72; Conservative
CURRENT APPLICATION DATA:
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Sequence 91, Application US/08454557C

Sequence 91, Application US/08454557C

Sequence 91, Application US/08454557C

Sequence 91, Application US/08454557C

Sexeral Information:

APPLICANT: de la Monte, Suzanne

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Pox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION INDER: 36,203
RECEPERNCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91: SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Search completed: June 15, 2000, 13:18:30 Job time: 87840 sec

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64.8
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                                                                                                                                               June 15, 2000, 13:12:08; Search time 17972.2 Seconds (without alignments) -1569.757 Million cell updates/sec
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29001
1 TIGTATTTTATTAGAGACA.......GCCTCAGCCTTCAGAGTGTA 29001
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   882769 seqs, -486395729 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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9b_bal: *
9b_bal: *
9b_ov: *
9b_ov: *
9b_ov: *
9b_pl: *
9b_pl: *
9b_pl: *
9b_pl: *
9b_pl: *
9b_pr: *
em_bun: *
em_bun: *
em_bun: *
em_bun: *
em_bun: *
em_bun: *
em_bat: *
em
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Maximum DB seq length: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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Database :

Sequence:

Run on:

Searched:

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gb_htg12:*
gb_htg13:*
gb_htg14:*
   em_htg1:*
em_htg2:*
em_htg3:*
em_htg3:*
                     gb_pl3:*
gb_pr5:*
gb_htg8:*
                                  gb_htg9:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human c	Human	XO5250 Human LDL-T XO5250 Human LDL-T	TIEBLE C	Human	Human	U67803 Human small	9 Human	X05251 Human LDL-r	9 Human	1 Human	Human	Human	8 Human	Human	Human	Human	Human		G32743 A009P31 Hum				VEZZOO HUMBIN LOW G	Human A	Human	Human c	Human	7 Human	M36135 Human alpha	6 Нишап	Human	Human a	Human	4 Human	Human a			5 WIAF-	Human f	S73203 ALL-1 [tand	D16965 Human HepG2	AF032287 Eulemur m
ID	HUMALCE162	HSU67803	HSLDLRN2 HSLDLRN2	HIMALCETES	HUMAI CE221	HUMALCE221	HSU67803	HSLDLRD1	HSLDLRD2	HSLDLRD1	HSLDLRD2	HSLDLI12	HSU67804	HSU67808	HUMALCE43	HUMALCE272	HUMLDLRA2	HUMALCE43	HSU67808	G32743	HS067807	HUMD1D03M5	HSLDLIIZ	HUMLDLKFL	100T000	HUMUT8164A	HUMALCE272	HSU67806	HSU67807	HUMBRKFAE	HSU67806	HUMBRKFAE	HUMHGAL	HUMUT8002B	HUMUT8164A	HUMHGAL	HUMUT8002B	HSBICBR	G43535	HUMLDLRDJ	873203	HUMD1D03M5	AF032287
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                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7316 GGCAGGAGAATGGCGTGAACGCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCATG 7375
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107)

2 (bases 1 to 107)

3 (bases 1 to 107)

Alu RNA transcripts in human embryonal carcinoma cells. Model opst-transcriptional selection of master sequences

J. Mol. Biol. (1992) in press

Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 108)
                              HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
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                                                                                               Alu repeat.
Homo sapiens male embryo carcinoma CDNA to other RNA
Homo sapiens
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Human small cytoplasmic Alu transcript.
U67803
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/db_xref="taxon:9606"
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/note="scalu"
/rpt_family="alu"
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)

1 (bases 1 to 108)

1 Horsthemke, B., Balsaiegel, U., Dunning, A., Havinga, J.R., Milliamson, R. and Humphries, S. Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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Human LDL-receptor gene intron 14 fragment (normal gene).
X05250
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Best Local Similarity 89.5%; Pred. No. 3.1e-07;
Matches 94; Conservative 0; Mismatches 11;
                                                                                                                     Score 89; DB 11; I
Pred. No. 1.5e-07;
0; Mismatches 5;
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/db_xref="taxon:9606"
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/note="intron XIV fragment"
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/rpt_type=dispersed
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Matches 92; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base) 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Blol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7286 GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGATGGCGTGAACGCGGGAGGCG 7345
                                                                                                                                                         Homo sapiens male embryo carcinoma cDNA to other RNA.

Homo sapiens
Bukaryota; Martazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model
post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
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Pred. No. 4.7e-06;
0; Mismatches 11;
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Pred. No. 2.3e-06;
0; Mismatches 10
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/sex="male"
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27 c 33 q 1
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27 c 33 q 1
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/cell_line="NTera2D1"
/dev_stage="embryo"
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88.9%;
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                                                                                                                       M87896.1 GI:174874
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Best Local Similarity 89.9
Matches 89; Conservative
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Best Local Similarity 88.9
Matches 88; Conservative
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1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
Bur. J. Blochem. 164 (1), 77-81 (1987)
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Homo sapiens
Bukaryota:
Homo sapiens
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcriptis in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) in press
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 4.1e-07;
0; Mismatches 12;
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Pred. No. 7.7e-07;
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23 c 39 g 18 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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30 c 35 g 1
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Best Local Similarity 88.7%;
Matches 94; Conservative
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illarity 89.3%;
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Shalkh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Shalkh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Submitted (25 Junisation of Human Genetics and Molecular Biology, The Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
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Human LDL-receptor mutated gene with intron 12 deletion junction
X05249
X05249.1 GI:34335
             14379 CTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTGTCTCCAGGGTTCAAGCGAT 14438
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                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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Eukaryota: Metazoa: Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
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                                                                                14439 TCTCCTGCTTCAGCCTATGGAGTAGCTGGGATTACAGGC 14477
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89.7%; Pred. No. 5.6e-06;
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                                                                                                   43 TCTCCTGCCTTAGCTTCCGTGTAGCTGGGATTACAGGC 5
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Human small cytoplasmic Alu transcript.
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/db_xref="taxon:9606"
/clone="TscAlu2"
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39 c 30 g
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/note="scAlu"
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*source: hypercholesterol aemia sequence Ses X05250 for corresponding normal gene sequence in the defective LDL-receptor gene the deletion courred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                              See X05248 for corresponding normal gene sequence. In the defective LDL-receptor gene the deletion occurred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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1 (bases 1 to 108)

Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia

Eur. J. Biochem. 164 (1), 77-81 (1987)
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//db_xref="taxon:9606"
//cell_type="blood leukocytes from a patient with familial"
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Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
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Alu repetitive sequence; low density lipoprotein receptor.
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85.6%; Pred. No. 8.8e-06;
tive 0; Mismatches 15; Indels
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Blochem. 164 (1), 77-81 (1987)
(bases 1 to 108)
HORSTHERMEN, B., Beislegel, U., Dunning, A., Havinga, J.R.,
HAISTHERMEN, B., Beislegel, U., Dunning, A., Havinga, J.R.,
HAILliamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
BTI J. Biochem. 164 (1), 77-81 (1987)
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
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Pred. No. 1.1e-05;
0; Mismatches 16;
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/db_xref="taxon:9606"
complement(<1. .65)
/note="Alu repeat"
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See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
allurepetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 14 deletion junction.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
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      0.3%; Score 80; DB 10; Length 108;
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                                       Pred. No. 8.8e-06;
                                                                       0; Mismatches
                                   85.6%;
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HSLDLRD1/c
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                                                                        9677 TCGGCTCACCGCAACCTCCGCCTCCAGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCCA 9736
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                                                                                           2 TCGCTCACCACAACCTCTGCCTCCTGGGTTCAAACCATTTTCCTGCCTCAGCCTTA 61
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1 (bases 1 to 108)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                        Gaps
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Pred. No. 2.4e-05;
0; Mismatches 12; Indels 0
Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 108)
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
                                                                                                                                               9737 GTAATTGGGACTACTGGCAAGCGCCACCACGCCTGGCTAATTTTGTA 9783
Score 78.2; DB 10; Length
Pred. No. 2e-05;
0; Mismatches 18; Indels
                                                                                                                                                                  Indels
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Human small cytoplasmic Alu transcript.
UG7808 GI:2289922
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Human small cytoplasmic Alu transcript.
U67804
U67804.1 GI:2289918
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/db_xref="taxon:9606"
/clone="TscAlu3"
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Best Local Similarity 87.6%;
Matches 85; Conservative (
Query Match 0.3%;
Best Local Similarity 83.2%;
Matches 89; Conservative
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Shaikh, T. H., Kim, J., Batzer, M. A. and Deininger, P. L.
Direct Submission
Submitted (12-AUG-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
1. .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 108)
Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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88.3%; Pred. No. 4.4e-05;
tive 0; Mismatches 11;
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/db_xref="taxon:9606"
/clone="TscAlu7"
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/rpt_type=dispersed
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Matches 83; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries

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Human gene signature HUMGS06998.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell typing; abnormal cell function; ss. Homo sapiens.
                    T25218
T25848
N60231
Q75099
X12087
T23513
T22572
Q69409
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Matches 78; Conservative
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01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences to double-stranded DNA) which comprises one of the 7837 "GS" sequences given in Ti9001-T26837 and which is able to hybridise to part of part of the man genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA mas initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library call fferent mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequence) as a means of diagnosing abnormal cell function or for crecognising different cell types. 28 T; 28 T;
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Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism, biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
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New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease testing or phenotypic typing for disease claim 1; Page 219; 310pp; English.
                               Human gene signature HUMS/09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

WO9514772-Al.
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2182; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X12095 standard; DNA; 108 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2811 CACGAGGTCAGGAGATC 2827
                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.2
Best Local Similarity 90.9
Matches 70; Conservative
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                                                                                                                                                                                             01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                             Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; marker; ss.
                                                                                                                                                                                                                                                                         (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                               WPI; 95-206931/27
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WO9820165-A2.
                          14-NOV-1996
                                                                                                                                                                                                                                                                                                                               Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissues
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x10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in x09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in ethods for determining polymorphic forms in an individual for use in c.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spendorned, osteogenesis inperfects, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such can long or therapeutic treatments. The isolated polymorphic nucleic acid drugs or therapeutic treatments. The isolated polymorphic nucleic acid sequence 108 BP; 19 A; 23 C; 28 G; 37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A single-stranded DNA (or its complementary strand or the corresp.

A single-stranded DNA, which comprises one of the 787 "63" sequences
double-stranded DNA, which comprises one of the 787 "63" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
cuntranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
c sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9780 TGTATTTTATTAGAGATGAGGTTTCTCCATGTTGGTCAGACTGGTCTCGAACTGCCGAC 9839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 108;
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81.5%; Pred. No. 0.0037;
tive 1; Mismatches 1
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Human gene signature HUMGS06998.
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hes 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OKUB/) OKUBO K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1994; J01916.
12-NOV-1993; JP-355504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 95-206931/27
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T20927 standard; cDNA to mRNA; 103 BP.
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RESULT
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                                                                                      NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For indian 37; Page 18; 60pp; English.

Compared shown in V41230 to V41247 represent nucleotide sequences of sequences shown in V41230 to V41247 represent nucleotide sequences of mouse EST from tagged cDNA clones. These are used in the method of the invention of screening for human developmental genes. The method comprises inserting a promocterless reporter gene into a non-primate comparison that encode the reporter gene product. Fragments of genes encoding these transcripts are cloned and sequenced. A gene encoding a transcript that includes unknown sequences is selected and expression clevel of the gene encoding the transcript, or part of it, in different cell types and/or different developmental stages is detected. A gene showing differential expression is selected and expression levels of a commologous non-human primate gene, in different cell types and/or at differential expression is selected and expression levels of a confiferential expression is selected and the non-primate transcript as comprehe is detected. A homologous gene having the same pattern of clifferential expression is selected and the non-primate gene, or part of it is used to identify the homologous human gene. The ESC transcripts clentified by this method are used to generate transgenic animals selected from rats, hamsters, rabbits, dogs, pigs, horses, cows, monkey, babbon or chimapanzee for study of gene function. The method provides crapid and large scale screening for human developmental genes, and celiminates the need to analyse reporter gene expression in embryos. Sequence 86 BP; 16 A; 28 C; 30 G; 12 T;
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                                                                                                                                                                   2943 ATGGCATGAACCTGGGAGGGGGAGCTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAA 3002
                                                                                                              Gaps
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                                                                                                                                                                                                     2 ATCGCTTGAACCTGGGAGGCAGAATTTGCAATNAGCTGAGATTGCACCNTTGCACTCCNG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for human developmental genes - by trapping in murine embryonic stem cells and analysing differential expression in vitro, selecting homologous non-human primate gene and using it to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CTGCTGGGCCGTGTGACCATCGCGCAGGCGGCGTCCTGCCCAATATCCAGGCCGTGCTG
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0
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                                                 Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-071-1998 (first entry)
Mouse embryonic cell EST 13-4 nucleotide sequence.
Embryonic stem cell; ESC; non-primate; mouse; EST; human; developmental gene; transgenic animal; reporter gene; sa.
                                                                                                           22; Indels
                                                                                                                                                                                                                                                                                           3003 CCTGGGAGACACAGGGAGACTCCGTCTCAAAAAAAAAA 3041
                                                                                                                                                                                                                                                                                                                         Score 65.6; DB 1 Pred. No. 0.0058;
                                                                                                        0; Mismatches
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25-NOV-1997; U22335.
27-NOV-1996; US-032510.
(CORR ) CORNELL RES FOUND INC.
                                                 0.28;
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Best Local Similarity 85.55
The Conservative
                                                                                                        77; Conservative
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WPI; 98-322656/28.
                                                    Ouery Match
Best Local Similarity
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WO9823633-A1.
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A single-stranded DNA (or its complementary strand or the corresp.
Claim 1; Page 758-759; 2245pp; Japanese.
Claim 1; Page 758-759; 2245pp; Japanese.
Caduble-stranded DNA (or its complementary strand or the corresp.
Caduble-stranded DNA) which comprises one of the 737 "63" sequences
Cyton in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
Sequences were obtained from 3'-directed CDNA libraries prepared
Cfrom various human tissues; synthesis of CDNA was initiated from the
Cfrom various human tissues; synthesis of CDNA was initiated from the
Cfrom various human tissues; synthesis of CDNA was initiated from the
Cfrom various human tissues; synthesis of CDNA was initiated from the
Cfrom various human tissues; synthesis of CDNA was initiated from the
Cfrom various human tissues; synthesis of CDNA was initiated
Cfrom various human tissues from which it was derived.
Cfrom various human tissues from which it was derived.
Cfrom papearance frequency of a given GS in a cDNA library can be
Cfrom various manns of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8631 GATTCTACTGCCTCGCCCTCCCGAGTAGCTGGGACCACAGATACGTGCCACGATGCCCCG 8690
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Human gene signature HUMGS02180.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Pred. No. 0.018;
); Mismatches 24; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CTGATTTTWGTATTTTWAGTAGGACAGTATTTCTCCATG 100
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Sequence 103 BP; 22 A; 27 C;
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Human gene signature HUMGS07131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-35564.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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Best Local Similarity
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WPI; 95-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsubara K, Oku
WPI; 95-206931/27
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17 T;

24 G;

recognising different cell types. Sequence 93 BP; 25 A; 27 C;

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                                                                                                                  A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
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Claim 1; Page 1907; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3-directed CDNA libraries prepared from various human tissues; synthesis of cDNA was intitated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA sceies, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of the appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reflects relative abundance of corresp. mRNA in specific human tissues
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Human gene signature HUMGS07887.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

HOMO Saplens.
                       for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA tha
Identifying gene signatures in 3'-directed human cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2%; Score 61; DB 1; Length 108; Best Local Similarity 74.5%; Pred. No. 0.036; Matches 76; Conservative 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8592 ATCTCGGCTCACTGCAACCTCCGCTTCCCAGGTTCAAGCGAT 8633
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                                                                                                Claim 1; Page 1748; 2245pp; Japanese.
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ID T25688 standard; cDNA to mRNA; 93 BP.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA libraries prepared from various human tissues; synthesis of cDNA instance from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
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                                                                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
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                                               20; Indels
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      DB 1;
  Score 60; DB 1;
Pred. No. 0.052;
                                                                                                                                                                              QY 11175 ACTGCAACCTCCGCCTCCTGGGTTCAAGGGAT 11206
                                               0; Mismatches
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Human gene signature HUMGS07131.
0.2%;
                        Best Local Similarity 78.3
Matches 72; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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      Query Match
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RESULT T26288 S

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double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
sequence 110 BP; 22 A; 28 G; 17 T;
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10-OCT-1996 (first entry)
Human gene signature HUMGS08527.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
Homo sapiens.
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Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-blased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
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T25260/c
T75260 standard; DNA; 110 BP.
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MAYEZ) MATEUBARA K.
(OKUBZ) OKUBO K.
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12-NOV-1994; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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95-206931/27.
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WPI; 95-206931/27.
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Best Local Similarity
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 787 "63" sequences couple-stranded DNA) which comprises one of the 787 "63" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA specific all the 3'-oriented cDNAs hybridise with specific mRNAs. Bach library all constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (asp. using primers and probes derived from the GS crecopising different cell types.
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14-NOV.)
14-NOV.
14-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.4; DB 1;
Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T26828 standard; cDNA to mRNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9667 TGGTGCGATCTCGGCTC 9683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TGGTGCCATCTCGGATC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsubara K, Okubo
WPI; 95-206931/27.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9514772-A1.
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F26213 standard; cDNA to mRNA; 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hudson T, Lander ES, Wang D, Waller B. Wal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                            52 AACTCCTGACCTCATGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGATTACAGGTGTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism, biallelic; human: forensic; paternity testing; disease;
detection: phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                              Gaps
                                                                                                                                                                                                                         2 ATCTCCTGACCTCGTCATCGCCCGTNTCGCCCTCCCATAGTGCTGGGNTTACAGGCATG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24966 AGACCAGCCTGGCCAATATTGTGAAACCCCGTCTCTACTAAAAAAA 25013
                                        DB 1; Length 108;
                                                                                                       22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 AGACCATCCTGGCCAACAYAGGAAAACCTCATCTCTACAAAAAGACA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 G;
                                                                     0.17;
                                 0.2%; Score 57; DB
75.8%; Pred. No. 0.17
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                     112 AGCCACTGCACCGGCCTTATTTTGCCTTCT 142
                                                                                                                                                                                                                                                                                                                                                             62 AGCCACGCCCGGCTGTTTATTTCTTAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WHED ) WHITEHEAD INST BIOMEDICAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
X12095/C
ID AC X12095 standard; DNA; 108 BP. AC X12095/C
ID 30-MAR-1999 (first entry)
DE Human biallelic polymorphic DNA
W Polymorphism; biallelic; human; detection; phenotypic typing; cly
W treatment; marker; ss.
NW WO9820165-A2.
PD 14-MAX-1996
ID 14-MAX-1997; UZ0313.
PR (G-NOV-1996; US-030455.
PR (WHED ) WHITEHEAD INST BIOMEDIC!
PI HUGSON T, Lander ES, Wang D;
NW 15094-286974/25.
PT (G-NOV-1996; US-030455.
PT (WHED ) WHITEHEAD INST BIOMEDIC!
PT (G-NOV-1996; US-030455.
PT (G-NOV-1996; US-030456.
PT (G-NOV-1906; US-030456.
PT (G-NOV-1906; US-030456.
PT (G-NOV-1906; US-030456.
PT (G-NOV-1906; US-030
                                                                                                              Conservative
                                                                         Similarity
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Matches 82; Conserv
                                                                                                          69;
                                        Query Match
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                                                                             Best Local
                                                                                                       Matches
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RESULT 14

T26213/c

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of part of them of the T19001-T26837 and which is able to hybridise to part of them of the T19001-T26837 and which is able to hybridise to part of them o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14338 TTTTTTTTTTTTTTTGAAATGGAGTTTCGCTCTTGCCCAGGCTGGAGTGCAGTGGCACAGA 14397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 TITITITITICITAAAGACATGIICITACICIGIGGCCCAGGCTGGAGIGCAGTGCTGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1996 (first entry)

Human gene signature HUMGS08978.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
13-NOV-1996 (first entry)
Human gene signature HUMGSO8452.
Gene signature, messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 95-206931/27. ... definition of the standard of secondard of secondard of secondard of secondard of secondard of corresp. mRNA in specific human reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY 14398 TCTCGGCTCACTGCAACCTCTGTCTCCAGGGTTCAAGCGAT 14438
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0; Mismatches
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Best Local Similarity 72...
Best Local 3; Conservative
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K. Okubo K;
                                                                                                                                                                                                                                                                                                                    11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsubara K,
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 [68] sequences double-stranded DNA) which comprises one of the 7837 [68] sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA hibraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-enterted sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 97 BP; 19 A; 27 C; 20 G; 28 T;
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ö 0; Gaps Query Match 0.2%; Score 54.8; DB 1; Length 97; Best Local Similarity 73.9%; Pred. No. 0.41; Matches 68; Conservative 0; Mismatches 24; Indels

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Qy 14633 CCAGGAGCAGATTTTTTACACTCATGTTTCT 14664

61 NCTGTACTAAGTCTTTTTTTTTTAAATTTCCT 92

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Search completed: June 16, 2000, 00:47:51 Job time: 128982 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq length: 110
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1127 Std Broor: 0.00
Seq primer: Jan Std Broor: 0.00
Insert Length: J
            Washington University School of Medicine
 Contact: Wilson RK
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AA703692 ag81al0.r
AA897366 am06h02.s
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AQ582186 RPCT-11-4
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AA228795 nc14e07.s
AQ637292 RPCI-11-4
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AA5370029 EST81584
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N49638 yv25e09.r1
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AA812141 ob48h02.s
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1 (bases 1 to 109)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Leinon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Walter, T., Waterston, R. and Wilson, R. Unpublished (1997)

On Dec 3, 1996 this sequence version replaced gi:1126869.
Description
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/db_xref="Taxon:9608"
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/clone="IMAGE:664467"
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

El (Abases I to 100 M)

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptce,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

L Onpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1397630.

Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@tmage.llnl.gov) for further information.
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                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 163)

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Morreth, J., Morre, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Waterston, R. and Wilson, R. Washu-NCI human EST Project

Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1133644.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
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/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT/T3D-Pac (Pharmacia) with a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at72g09.x1 Barstead colom. HPLRB7 Homo sapiens cDNA clone IMAGE:2377600 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence. AIB32832. GI:5454812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2377600"
/clone_lib="Barstead colon HPLRB7"
/sex="male"
Seq primer: -28ml3 revl ET from Amersham High quality sequence stop: 53. Location/Qualifiers
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria: Prinates; Catarrhini; Hominidae; Homo.

Eutheria: Prinates; Catarrhini; Hominidae; Homo.

Eutheria: Prinates; Catarrhini; Hominidae; Homo.

Endams.M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Ṣuh,E., Wible,C., de Jong,P. and
Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building

Contact: Mark Adams

Contact: Mark Adams

Department of Enkaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Closes are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pleteredejong.med.buffalo.edu). Clones may be purchased from Research Genetics (http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
/col_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
1 28 c 30 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9627 GAGACGGAGTTTCACACTTGTTGCCCAGGCTGGAGTGCAATGGTGCGATCTCGGCTCACC 9686
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.12;
0; Mismatches 7; Indels 0
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/db_xref="GDB:7501163"
/db_xref="taxon:9606"
/clone="RRCI-11-4A12"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 93.3%;
Matches 98; Conservative
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Gaps

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Query Match Best Local

Matches

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RESULT 5 AA812141/C

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LOCUS DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/note-"vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned 51ze-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 107)

INCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:1899815.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergaih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     od71a07.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1373364 similar to contains Alu repetitive element; contains element MER22
                                                                                                              GGAGAATGGCGTGAACGCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCATGGCAC 7379
                                                                                                                                                                                106 GGAGAATGGTGTGAACCTGGGAGGTGGAGCTTGCAGTGAGCCGAGATCACACCACTGCAC 47
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High quality sequence stop: 93.
Location/Qualifiers
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                                    Mismatches
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/clone="IMAGE:1373364"
/clone_llb="NCI_CGAP_Ov2"
           Pred. No.
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/lab_host="DH10B"
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       91.5%;
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Carald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA812141 106 bp mRNA EST 19-FEB-1998 ob48h02.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1334643 3/ similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1402063.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                               2774 GTAATCCTAGCACTTTGGGAGGCCGAGACGGGCGGATCACGAGGTCAGGAGATCGAGACC 2833
                                                                                                                                                                                   Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Length 103;
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/clone_lib="NGI_CGAP_GCB1"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                       2834 ATCTTGGCTAACACGGTGAAACCCCGTTTCTACTAAAATACA 2876
                                                                                                                                                                                                                                                                                                                               61 ATCCCGGCTAAAACGGTGAAACCCCGTCTCTACTAAAAATACA 103
       DB 84;
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Score 91.8; DB Pred. No. 0.21; 0; Mismatches
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                                        93.28;
                                                                         96; Conservative
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source

FEATURES

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Gaps
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                                              2922 TTGGGAGGCTGAGGCAGGAGTGGCATGAACCTGGGAGGCGGA 2965
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Query Match

BASE COUNT

ORIGIN

0.3%; Score 91.2; DB 39; Length 107; 92.3%; Pred. No. 0.24;

LOCUS DEFINITION

AA243009

RESULT

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ACCESSION KEYWORDS SOURCE

VERSION

ORGANISM

AUTHORS REFERENCE

TITLE JOURNAL COMMENT

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3'); double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI: 1st strand cDNa was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N25299 109 bp mRNA EST 28-DEC-1995
yw52c09.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone
IMAGE:255856 3' slmilar to contains Alu repetitive element;, mRNA
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1 (bases 1 to 101)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu' NCI human EST Project
On Nov 29, 1993 this sequence version replaced gi:636191.
element; contains element KER repetitive element ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7313 TGAGGCAGGAGAATGGCGTGAACGCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCC 7372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Barstead pancreas HPLRB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7373 ATGGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGTCTCA 7413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89.8; DB 39;
Pred. No. 0.35;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult, 34 years"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:1412689"
                                                                    AA835205.1 GI:2908933
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/clone_lib="Stratagene NT2 neuronal precursor 937230"
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/deb_host="sOLR (kanamycin resistant)"
/deb_host="sOLR (kanamycin resistant)"
/dep_nosting neuroepithelial
/dev_stage="neuroepithelial"
/dev_stage="neuroepith
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                                                                                                                                                                       AA243009 109 bp mRNA EST 11-MAR-1998 ZZ25N02.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664467 3' similar to contains Alu repetitive element; contains element LTR1 repetitive element; n mRNA sequence. AA243009
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1 (bases 1 to 109)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wnite,Y., Wylie,T., Waterston,R. and Wilson,R. Wash-NCI human EST Project

On Dubulishad (1997)

On Dec 3, 1996 this sequence version replaced gi:1126869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoeimage.llnl.gov) for further information.
Insert Length: 1127 Std Error: 0.00
Seq primer: -41al3 fwd. ET from Amersham
High quality sequence stop: 102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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64 TTGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGA 107
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Pred. No. 0.22;
0; Mismatches 11;
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/db_xref="GDB:5426481"
/db_xref="taxon:9606"
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Best Local Similarity 89.9%;
Matches 98; Conservative (
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1 (bases 1 to 109)

Chissoe, S. Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Cholfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,

and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N49638 97 bp mRNA EST 14-FEB-1996 yv25e09.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243784 5' similar to gb:X57138_rnal HISTONE H2B.2 (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mi3 -40 forward
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
                                                                                                                                                                                             On Apr 14, 1993 this sequence version replaced gi:837394.
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                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.32;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="CDB:3866265"
/db_xref="taxon:9606"
/clone="IMAGE:255856"
/clone_lib="Weizmann Olfactory Epithelium"
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N49638
N49638.1 GI:1190804
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les 96; Conserv
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                     AUTHORS
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pr773D (Pharmacla)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5. AACTGGAAGAATTAAAGARCTTTTTTTTTTTTTTTTTTT] 3'],
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 103)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
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Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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On Apr 14, 1993 this sequence version replaced gi:693230.
Contact: Wilson RK
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 97;
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Pred. No. 0.37;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: T7
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                  The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Unpublished (1998)
Contact: Mark Adams
Contact: Mark A
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Seg primer: M13-21
Class: BAC ends.
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
a 30 c 34 g 17 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7323 GAATGGCGTGAACGCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCGCCATGGCACTCC 7382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ264176 106 bp DNA GSS 27-OCT-1998 CITB1-E1-2509A2.TF CITB1-E1 Homo sapiens genomic clone 2509A2, genomic survey sequence.
AQ264176 GI:3792743
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                                                                                                                                   /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No. 0.52;
0; Mismatches 8; Indels 0
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                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2363C23"
/clone_lib="CIT-HSP"
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/db_xref="taxon:9606"
/clone="2509A2"
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/sex="male"
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Best Local Similarity 92.1%;
Matches 93; Conservative
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: mdadamsetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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                 Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
10 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: Maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 101)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, B., Wible, C., Shizuya, H., Simon, M. and
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Seg primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No. 0.46;
0; Mismatches 9; Indels 0;
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/db_xref="taxon:9606"
/clone="2323P12"
Other_GSSs: CIT-HSP-2323P12.TF
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1. .103
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Best Local Similarity 91.3%;
Matches 94; Conservative (
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AW250394
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Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

1 (bases 1 to 103)

1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

1 NGI-CGAP institute, Cancer Genome Anatomy Project (CGAP),

1 Tumor Gene Index

1 Unpublished (1997)

2 On Jan 19, 1998 this sequence version replaced gi:2151346.

2 Contact: Robert Strausberg, Ph.D.

2 Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

7 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DAS Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MCI-CGAP clone distribution information can be
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                                                                                                                                           2812 ACGAGGICAGGAGATCGAGACCATCTTGGCTAACACGGTGAAACCC 2857
                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1255473"
/clone=lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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  89.6%; Pred. No. 0.48;
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91.2%; Pred. No. 0.6;
tive 0; Mismatches
                     0; Mismatches
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CONTEX_ESTS: 221240.3PTIME
CONTEXE.STS: 221240.0.5PTIME
CONTEXE. Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Tel: (301) 496-1550

Trissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP CDNA Library Arrayed by: The I.M.A.G.E.
CONSORTIUM (LINL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. ConSortium/Linl at:
www-bio.llnl.gov/bbrp/image/image.html Base calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross_match from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: parMatch, pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 61
contiguous PHRED high quality bases following vector sequence. Nery
Low Quality Sequence: Trace file contained 110 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
propresence.
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/tissue_type="small cell carcinoma"
/tissue_type="small cell carcinoma"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage_resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                     AW250394 110 bp mRNA EST 07-JAN-2000
2822460.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822460 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138342.
Other_ESTs: 2822460.5prime
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
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Pred. No. 0.58;
0; Mismatches 14;
43 TCGAGACCATCCTGGCTAACACGGTGAAACCCCATCTCTACT
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/db_xref="taxon:9606"
/clone="IMAGE:2822460"
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High quality sequence stop: 61.
Location/Qualifiers
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AW250394
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Search completed: June 15, 2000, 19:11:36 Job time: 110063 sec

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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.3E
TELEPHONE: 415-435-073
TELEPHONE: 415-435-072
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDENESS: SINGLE
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Pred. No. 2.5e-09;
US-08-340-426D-57
US-08-450-673C-57
US-08-45-557C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-454-557C-60
US-08-450-673C-60
US-08-450-673C-60
US-08-450-673C-60
US-08-450-673C-60
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-70
US-08-450-673C-70
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Sequence 65, Application US/08481658B
Sequence 65, Application US/08481658B
SEREAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                    ALIGNMENTS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
   COMPUTER READABLE FORM:
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: USA
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US-08-481-658B-65
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   June 15, 2000, 13:18:30 ; Search time 373.9 Seconds (without alignments) 10082.098 Million cell updates/sec
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                                                                                                                                                                                                                                                    374504
                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/Packfiles1.seq:*
7: /cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-340-426D-92
US-08-450-673C-92
PCT-US95-17111A-92
US-08-454-557C-57
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US-08-486-756A-65
US-08-486-8628-65
US-08-481-658B-65
US-08-481-658B-65
US-08-481-658B-65
US-08-486-758A-65
US-08-787-739-65
US-08-787-739-65
US-08-340-4260-91
US-08-450-673C-91
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US-08-454-557C-91
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PCT-US95-17111A-91
US-08-454-557C-92
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US-08-454-557C-69
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US-08-450-673C-69
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                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           230463 segs, 64992525 residues
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                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 110
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760.2
776.2
776.2
776.2
776.2
776.2
760.2
633.8
633.8
653.8
653.8
653.8
653.8
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US-08-486-756A-65
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       0; Gaps
                                                                                  1 TTGTATTTTATTAGAGACAGGGTTTCACTATGTTGGCCAGGCTGATCTCAAACTCCTGA 60
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CURRENT APPLICATION DATA:

APPLICATION NOMBER: US/08/477,504A

FILING DATE: 07-UNY-1995

CLASSIFICATION A74

PRIOR APPLICATION DATA:

APPLICATION NOMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGRAT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: D-0021.3D

FELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNI
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       0; Mismatches 13; Indels
                                                                                                                                                                                                                                  61 CCTCATGATCCGCCTGCCTTGGCCTCTCAAAGTGCTGGGAT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mailposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-477-504A-65
Sequence 65, Application US/08477504A
Patent No. 5972353
GENERAL INFORMATION:
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
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US-08-477-504A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION 244
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 CCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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; Sequence 65, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
CITY: Tiburon
COUNTED COURTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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Patent No. 5989838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     USA
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US-08-486-756A-65
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Query Match
Best Local Similarity 87.19
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LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-981-0332 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TTACATCTTTAGTAGAGACAGGGTTTCACCATATTGGCCAGGCTGCTCTCAAACTCCTGA 64
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                                                                    COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/477,504
APPLICATION NUMBER: US 08/477,504
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona I
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELEPONNE: 415-435-2034
TELEPANONE: 415-435-2034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCTCATGATCCGCCTGGCCTTGGCCTCTCAAAGTGCTGGGAT 101
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Fatent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
APPLICANT: Pastorek, Jaromir
APPLICANT: Pastorek, Jaromir
APPLICANT: Pastorek, Jaromir
APPLICANT: Apple Street, Suite 610
STREET: 369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 88; Conserv
                  USA
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                                      94920
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US-08-485-862B-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-787-739-65
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                  COUNTRY:
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0; Gaps
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87.1%; Pred. No. 2.5e-09;
tive 0; Mismatches 13; Indels
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Sequence 65, Application US/08481658B

Patent No. 5955075

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/41,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-0021.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lauder, Leona L. REGISTRATION NUMBER: 30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
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STREET: 6 Natiposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.3%
Best Local Similarity 82.9%
Matches 87; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-477-504A-65
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Pred. No. 2e-08;
0; Mismatches 18; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2837 TIGGCTAACACGGTGAAACCCCGTTTCTACTAAAAATACAAAAA 2881
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Sequence 65, Application US/08477504A
Sequence 65, Application US/08477504A
Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Talvia
STATE: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                       CURKENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 07-JUN-1995.

CLASSIFCATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

APPLORNEY AGENT INFORMATION:

NAME: Lauder, Leona L.

REFERENCE/DOCKET NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021,3E

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SEQ 1D NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.3%;
Best Local Similarity 82.9%;
Matches 87; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-481-658B-65
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2777 ATCCTAGCACTTTGGGAGGCCGAGACGGCGGATCACGAGGTCAGGAGATCGAGACCATC 2836
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SOFTWARE: PACENTE RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORREY/AGENT IRFORMATION:
NAMP: 15-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2837 ITGGCTAACACGGTGAAACCCCGTTTCTACTAAAAATACAAAAA 2881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-2034
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION:
TELEPHONE: 415-435-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-486-756A-65/c; Sequence 65, Application US/08486756A; Detent No. 5981711; GENERAL INFORMATION:
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2777 ATCCTAGGACTTTGGGAGGCCGAGACGGCCGGATCACGAGGTCAGGAGATCGAGACCATC 2836
                                                                                                                                                                                                Sequence 65, Application US/08787739 Patent No. 6027887 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-981-0332 INFORMATION FOR SEQ ID NO:
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STATE: California
COUNTRY: USA
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ANTI-SENSE: NO
US-08-787-739-65
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US-08-787-739-65/c
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STREET: 36
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                                                                                                       Score 76.2; DB 4; Length 105;
Pred. No. 2e-08;
0; Mismatches 18; Indels
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Pred. No. 2e-08;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALF: 94920
CAMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYZEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 107-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-0021.3D
                                                                                                                                                                                                                                                                                                                                                             US-08-485-862B-65/c; Sequence 65, Application US/08485862B; Patent No. 5989838; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFRENCE/DOCKET NUMBER: D-00:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-435-2034
INFORMATION FOR SEQ. ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYRE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 82.9%;
Matches 87; Conservative (
                                                                                                       Query Match 0.3%;
Best Local Similarity 82.9%;
Matches 87; Conservative (
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                                   ; ANTI-SENSE:
US-08-486-756A-65
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COMPUTER READABLE FORM:

MEDIUM TYFE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYFE: Floppy disk
COMPUTER: IMP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATIO
                                                                                                                                APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
AITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Leona L. Lauder
369 Pine Street, Suite 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lauder, Leona L.
RECISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
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GENERAL INFORMATION:
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US-08-450-673C-91/c
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                         2777 ATCCTAGCACTTTGGGAGGCCGAGACGGCGGATCACGAGGTCAGGAGATCGAGACCATC 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2767 CACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGACGGGCGGATCACGAGGTCAGGAGAT 2826
                                                               Gaps
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                Query Match 0.3%; Score 76.2; DB 5; Length 105; Best Local Similarity 82.9%; Pred. No. 2e-08; Matches 87; Conservative 0; Mismatches 18; Indels
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85.5%; Pred. No. 1.1e-05;
tive 0; Mismatches 12; Indels
                                                                                                                                                                                               2837 TTGGCTAACACGGTGAAACCCCGTTTCTACTAAAAATACAAAAA 2881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                       45 CTGGCCAATATGGTGAAACCCTGTCTACTAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEO ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-454-557C-91/C
Sequence 91, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-340-426D-91/c; Sequence 91, Application US/08340426D; Patent No. 5948634
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Best Local Similarity 85.5
Matches 71; Conservative
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Patent No. 594888
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R. TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: All Albeimer's Disease NUMBER OF SEQUENCES: 121 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2767 CACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGACGGGCGGATCACGAGGTCAGGAGAT 2826
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                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
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Pred. No. 1.1e-05;
0; Mismatches 12
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                                                                                                                                                                                                                                     STATE: COUNTRY: U.S.A.
ZOUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ludwig, Steven R.
REGISTRATION UNDBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFAM: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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Best Local Similarity 85.5%;
Matches 71; Conservative
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                                                                                                                                                                                                     Washington
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Indels

DB 6;

Score 63.8; DB 6; Pred. No. 1.1e-05; 0; Mismatches 12

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0.2%;
                                                                     Query Match
Best Local Similarity 85.58
Matches 71; Conservative
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STRANDEDNESS: both
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PCT-US95-17111A-91
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US-08-454-557C-69
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US-08-454-557C-69
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                            0.2%; Score 63.8; DB 4; Length 84;
85.5%; Pred. No. 1.1e-05;
tive 0; Mismatches 12; Indels
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ZIP: 20005-3934
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFRENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INPORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDIESS: both
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REGISTRATION NUMBER: 36,203
REFERENCE-DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 91:
LENGTH: 84 base pairs
               APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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FORT-0895-17111A-91/c
Sequence 91, Application PC/TUS9517111A
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 85.59
Matches 71; Conservative
CURRENT APPLICATION DATA:
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STRANDEDNESS: both
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STATE: D.C
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US-08-450-673C-91
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APPLICANT: Wands, Jack R.
TAPPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF ESQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8680 ACCATGCCCCGCTAATTTTTGTATTTTTAGTAGAACAGGGTTTCACCGTGTTGGCCAGG 8739
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                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 1.8e-05;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Stewen R.
REGISTRATION NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      Sequence 69, Application US/08454557C
patent No. 5830670
GENERAL INFORMATION:
2827 CGAGACCATCTTGGCTAACACGG 2849
                          23 CGACACCAGCCTGATGAACATGG 1
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Best Local Similarity 97.0%;
Matches 64; Conservative
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Search completed: June 16, 2000, 00:17:42 Job time: 127392 sec

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June 16, 2000, 00:11:20 ; Search time 17971 Seconds (without alignments) -1569.858 Million cell updates/sec
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29001
1 TTTTCCACTCTTCTTCAG......AGAGTGTTTGACCTCTAGGA 29001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                    OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 110
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Perfect score:
Sequence:
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gb_htg9:*
gb_htg10:*
gb_htg11:*
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Pred. No. is the number of results predicted by chance to have a score of greater than on equal to the score of the result being printed, and is derived by analysis of the feet of the result being printed,

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Searched:

Run on:

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2		HSLDLRN2	HUMALCE162	HSLULKUI HST DT BD3	HSI.DI.RN2	HUMALCE221	HSLDL112	HSU67803	HUMALCE162	HUMALCE221	HSLDLRD1	HSLDLRD2	HSBICBR	HSU67807		HUMALCE272	Σ	HSU67808	HUMLDLRA2	HSU67807	HSU67804	HUMUT7692A	HSLDL112	HUMUT8002B	G32614	879560	HSU67806	G43535	HUMLDLRFL	HUMUT8164A	873203	879560	HSSTHPKIB	643535		HUMUT8164A	HUMHGAL	HUMGALNSA	HUMGALNSA	HUMLDLRA2	HUMD1D03M5	HSU19407	HSLAS27	HUMALCE43	HUMLDLRFL
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& Query Match Length		108	107	108	108	103	108	108	107	103	108	108	103	110	103	104	108	108	97	110	108	66	108	95	108	101	107	108	90	91	6/	101	35	108	80	91	94	100	100	97	108	90	100	110	06
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HSLDLRD2
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                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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KEYWORDS
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1 (bases 1 to 107)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcriptis in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25347 ACAAAAATCAGCCAGGCGTGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAG 25406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
                                      20-MAY-1992
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
                                  HSLDLRN2 108 bp DNA PRI 20-MAY-1
Human LDL-receptor gene intron 14 fragment (normal gene).
X05250.
X05250.1 GI:34337
Alu repetitive sequence; low density lipoprotein receptor.
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                  See X05252 for deletion junction
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
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Pred. No. 1e-07;
0; Mismatches 5
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30 c 35 q 14
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/db_xref="taxon:9606"
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/sex="male"
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                                                                                                                                                                                                                                                                                                                    87161901
                                                                                                                              human.
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*source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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Human LDL-receptor mutated gene with intron 12 deletion junction.
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Human LDL-receptor mutated gene with intron 14 deletion junction.
X05251
                                                                                                       20076 ITTICTGAGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAATGCAGTGGCACAATCTCGGC 20135
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                                                                                                                                                        107 TITITIGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGC 48
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Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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Alu repetitive sequence; low density lipoprotein receptor.
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     Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
                                                      Indels
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                                                                                                                                                                                                                                       47 TCACTGCAAGCTCCGCGCTTCACGCCATCTTCTGCC 5
                                                      8
Score 90.2; DB 9;
Pred. No. 3.4e-06;
0; Mismatches 8;
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0.3%;
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Query Match 0.3
Best Local Similarity 92.2
Matches 95; Conservative
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Matches 96; Conserv
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ACCESSION
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HSLDLRD1/c
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Gaps

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MEDLINE COMMENT

FEATURES

JOURNAL

REFERENCE AUTHORS

TITLE

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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 108)

Horsthemke, B., Beislegel, U., Dunning, A., Havinga, J.R., Mylliamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Blochem. 164 (1), 77-81 (1987)
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Human LDL-receptor gene intron 12 fragment (normal gene) LDL = low
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Jose 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Blol. (1992) In press
Location/Qualifiers
                                            20130 CTCGGCTCACTGCAACCTCCGCCTCCCGGATTCACGCCATTCTCCTGCCTCAACCTCCCG 20189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25372 ATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAAGAGAATTGCTTGAACCCAGGA 25431
                                                                                                                                                                                                                                                                        HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Alu repetitive sequence; low density lipoprotein receptor;
repetitive sequence.
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Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
                                                                                                                                    20190 AGTAGCTGGGACCACAGGCGCCCGCCACCACGCCAGCTAATTTT 20235
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  12; Indels
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                                                                                                                                                            48 AGTAGCTGGGATTACAGGCACCTGCCACCACCACGCCTGGCTAATTTTT 3
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  Mismatches
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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  Conservative
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HSLDLI12/c
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VERSION
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SOURCE
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       Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, E. Williamson, R. and Humphries, E. Williamson, R. and Humphries, Dunary Crossing - Over between two alurepetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Bur. J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                             Securities: hypercholesterol aemia
Sec X05250 for corresponding normal gene sequence
In the defective LDL receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data Kindly reviewed (10-DEC-1987) by HUMPHRIES S.
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Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R., Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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Human LDL-receptor gene intron 14 fragment (normal gene).
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89.4; DB 10;
Pred. No. 4.6e-06;
0; Mismatches 11;
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Pred. No. 1.3e-05;
Primates; Catarrhini; Hominidae; Homo
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23 c 39 g 18 t
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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37 GCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20246 GTAGAGACAGGGTTTCACCGTGTTAGCCGGGATGGTCTCGATCTCCTGACCTCATGATCT 20305
                                                                                                                                                                                                                                                                              25350 AAAATCAGCCAGGCGTGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCA 25409
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
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            Data kindly reviewed (07-DEC-1987) by HUMPHRIES Location/Qualifiers
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                                                                                                                                                                                                               ch 0.3%; Score 83.2; DB 10;
1 Similarity 87.5%; Pred. No. 5.4e-05;
91; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                           45 GGAAAATGGTTTGAACCCAGGAGGCAGAGGTTGTGGTGAGGCGA
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llarity 90.7%; Pred. No. 6.9e-05;
Conservative 0; Mismatches 9;
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Human small cytoplasmic Alu transcript.
U67803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Mol. Biol. 271 (2), 222-234 (1997)
                                                                                                                                     /note="intron XII fragment"
38 c 20 g 29 t
                                         1. .108 /organism="Homo sapiens" /db_xref="taxon:9606" complement(<1. .65) /note="Alu repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
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/db_xref="taxon:9606"
see X05249 for deletion junction
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/rpt_type=dispersed
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1.108
/note="scAlu"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
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HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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Homo sapiens
                                                                                              Alu repeat.
Homo sapiens male embryo carcinoma cDNA to other RNA.
Momo sapiens
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Pred. No. 0.00012;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
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30 c 35 g 14
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Best Local Similarity 87.3%;
Matches 89; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE COMMENT

RESULT 11

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HSLDLRD1

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Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Biochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                  See X05250 for corresponding normal gene sequence. In the defective LDL-receptor gene the deletion ocurred between two alu-repetitive sequences, that are in the same direction, the deletion eliminates exons 13 and 14 and changes the reading frame of the resulting spliced MRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /--/b.zref="taxon:9606"
//cell_type="blood leukocytes from a patient with familial"
1..108
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Enimates; Catarrhini; Hominidae; Homo.

Aldridge, F.L.
Aldridge, F.L.
Submission
Submitted (12-FBB-1991) F.L. Aldridge, ICI Pharmaceuticals,
Alderley Park, Macclesfield, Cheshire, SK10 476, UK
(Dasses 1 to 103)
Butler, R. Riley, J. H., Ogllvie, D. J., Anand, R., Buxton, J.,
Davies, J., Johnson, K. and Markham, A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20131 TCGGCTCACTGCAACCTCCGCCTCCCGGATTCACGCCATTCTCTGCCTCAACCTCCCGA 20190
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                                       Dunning, A., Havinga, J.R.,
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Pred. No. 0.00025;
0; Mismatches 16;
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/clone="8IC8"
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/db_xref="taxon:9606"
/chromosome="19q13"
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   1 (bases 1 to 108)
Horsthemke, B., Beistegel, U., Du
Williamson, R. and Humphries, S.
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84.8%;
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Best Local Similarity 84.8'
Matches 89; Conservative
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarthini; Hominidae; Homo.

1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Williamson, R. and Humphries, S.
Williamson, R. and Humphries, S.
Williamson, R. and Humphries, F.
Williamson, B. and Humphries, F.
Williamson, B. and Humphries, B.
Williamson, B. and B.
Williamson, B.
Williamso
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See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion courred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data Kindly reviewed (07-DEC-1987) by HUMPHRIES S.
Location/Qualifiers
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/cell_type="blood leukocytes from a patient with familial"
1. 108
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Human LDL-receptor mutated gene with intron 12 deletion junction.
X05249
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                                                                                              20110 CTGGAATGCAGTGGCACAATCTCGGCTCACTGCAACCTCCGGCCTCCCGGATTCACGCCAT 20169
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m c} 20 g 28 t
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         103 CTGGAGTGCAATGCCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAT 44
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                                   Indels
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                                87; Conservative
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Matches 87; Conserv
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RESULT 12 HSLDLRD2/c

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Search completed: June 16, 2000, 08:46:10 Job time: 158854 sec
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Shalkh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Submitted (12,446-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                    13076 TGTCTGTAATACCAGCACTTTGGGAGGCCGATGTGGGGTGGATCACCTGAGGTCAGGAGTT 13135
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1 (bases 1 to 110)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
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85.7%; Pred. No. 0.0011;
tive 0; Mismatches 14; Indels 0;
   Length 103;
                                   16; Indels
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Human sequence tagged site 8ICBR DNA from 19q13.
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0.3%; Score 76; DB 13;
84.2%; Pred. No. 0.00095;
tive 0; Mismatches 16;
                                                                                                                                                                                                                                                          HSU67807 110 bp RNA
Human small cytoplasmic Alu transcript.
U67807.1 GI:2289921
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/db_xref="taxon:9606"
/clone="TscAlu6"
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Query Match 0.3%
Best Local Similarity 84.2%
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X57789.1 GI:23938
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Best Local Similarity 85.7°
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Length 103;
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/clone_lib="YAC library: ICI"
clone="81C8"
1 28 c 23 g 22 t
                                                                                                                                                                                                                                      /organism="Homo sapiens"/db_xref="taxon:9606"
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Location/Qualifiers
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Matches 83; Conservative
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Calaim 1: Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic typing for disease

Ca (1912-171268 and page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic are represented in markers which have been isolated using the primers represented in an expropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for diseases such as agammaglobulinemia, disbetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hemorrhagic telanglectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, such manner diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longewity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or contract or contract.
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                                                                             Human biallelic polymorphic DNA fragment TIGR-A003M18a.
Polymorphism, biallelic; human; forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
treatment; marker; ss.
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Human gene signature HUMGS06998.

Gene signature: messenger RNN; mRNA; relative abundance; frequency;

Gene signature: messenger RNNs; mRNA; relative abundance; frequency;

human; cloning; mapping; non-biased library; diagnosis; detection;

cell typing; abnormal cell function; ss.

HOMO saplens.

01-JUN-1994, JU1916.

11-NOV-1993; JP-355504.

(MATS/) MATSUBARA K.
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RESULT
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A single-stranded DNA (or its compolementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "Gs. sequences double-stranded DNA) which comprises one of the 7837 "Gs. sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA hibraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end in the particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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                               Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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WPI; 95-206931/27. ...
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy 28798 CCTGAGCAACACAGGGAGACTCTGTCTCAAAAAA 28832
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11-NOV-1994; JO1916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
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Best Local Similarity
WPI; 95-206931/27.
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A single-stranded DNA (or its complementary strand or the corresp.

Gouble-stranded DNA) which comprises one of the 7837 "GS" sequences given in 119001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 13'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence; sunique to a particular mRNA species, almost all the 3'-oriented cDNA hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (asp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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Human gene signature HUMGS06998.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
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                                                                                                                    Human gene signature HUMGS08084.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.2%; Score 59.4; DB 1; Best Local Similarity 77.5%; Pred. No. 0.38; Matches 69; Conservative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 G;
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                                                 T25854 standard; cDNA to mRNA; 91
                                                                                                22-OCT-1996 (first entry)
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                              01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSIBARA K.
(OKUB/) OKUBO K.
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WPI; 95-206931/27
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WO9514772-Al.
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WO9514772-A1.
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                                                                            T25854;
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T24892/c
       RESULT
T25854
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A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA, which comprises one of the 787 "GS" sequences

given in T19001-T26837 and which is able to hybridise to part of

human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)

sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of CDNA was initiated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

untranslated sequence is unique to a particular mRNA species, almost

call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

ceferanhoed (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                        25415 ATTGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAAATCGCGCCCACTGCACTCCAG 25474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19275 TTATTTTTTTTTGAGTCAGAGTCACACTCTGTCGCCCAGGCTGGAGTGCAGTGGCGTG 19334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Human gene signature HUMGS08452.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.
                             for
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    GS
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                                                                                                                                                  Length 108;
determined (esp. using primers and probes derived from the sequences) as a means of diagnosing abnormal cell function recognising different cell types.

Sequence 108 Bp; 34 Å; 31 C; 26 G; 15 T;
                                                                                                                                                                                                                                                                                                                                    Score 63.4; DB 1; Length 1
Pred. No. 0.094;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                               62 CCTGAGTGACAGAGCAAGACCTGTTGAAAAACAACAACAACAACAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recognising different cell types.
Sequence 103 BP; 33 A; 21
                                                                                                                                             0.2%;
                                                                                                                                        Query Match
Best Local Similarity 73.8%
Matches 79; Conservative
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Best Local Similarity 76.3
Matches 74; Conservative
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01-UUV-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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Gaps

15 T;

26 G;

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34

BP;

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                                                                                         A single-stranded DNA for its complementary strand or the corresp.

C double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed as oas to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1748; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26637 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-end of mRNA by using poly(") as the sole primer since the 3'-end of mRNA by using poly(") as the sole primer can be call the 3'-oriented cDNAs hybridise with specific mRNAs Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 TITGITIGITETTCAAACAGAGTGTCACTCTGTCACCCAGGCNGGAGTGCAANGGTGCAATC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1996 (first entry)
Human gene signature HDMGS07131.
Human gene signature: HDMGS07131.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
WO9514772-A1.
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for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                         Claim 1; Page 1720; 2245pp; Japanese.
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ID T25009 standard; cDNA to mRNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 73.7
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsubara K, Oku
WPI; 95-206931/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                     tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T25009;
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                                                                       20063 TTTTTTTTTTTTTTTCTGAGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAATGCAGTG 20122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20924 GATCACTTGAGTCCAGGAGTTTGAGACCAGCCTGGTCAACATGGCGAAACCTCATCTCTA 20983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lissues
Claim 1: Page 914: 2245pp: Japanese.
A single-stranded DNA (or its complementary strand or the corresp.
double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed CDNA libraries prepared
from various human tissues; synthesis of CDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-criented CDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                      Gaps
                                                                                             108 TITGNIGITGITGITGITGITTICAACAGGGTCITGCTCTGTCACGCTGGAAINCAGTG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATCGCTTGANCCCAGGAGTTTAAAACCAGCCCGAGGAACATGGCGAAACCCCATCTTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                    03-AUG-1996 (first entry)
Muman gene signature HUMGS02944.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               determined (esp. using primers and probes uerived it. ... sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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 Length 108;
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                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The appearance frequency of a given GS in a cDNA library determined (esp. using primers and probes derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
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 DB
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Score 58.6; DB Pred. No. 0.51;
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79.8%; Pred. No. 0.63;
tive 0; Mismatches
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T21566 standard; cDNA to mRNA; 87 BP.
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                                                                                                                                                                                                                                                                               T21566 standard; cDNA to mRNA; 87
T21566;
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0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WUDJ14,...
01-JUN-1995, J01916.
11-NOV-1994, J01916.
12-NOV-1993, JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                  76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
 Query Match
Best Local Similarity
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                                      Matches
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ID T215
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Claim 1; Page 2182; 2245pp; Japanese.
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C double-stranded DNA) which comprises one of the 7817 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of the man genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) ageneres were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cc untranslated sequence is unique to a particular mRNA species, almost all the 3'-orlanted cDNAA hybridise with specific mRNAs. Each library CC different mRNAs in the particular tissue from which it was derived. CC determined (esp. using primers and probes derived from the GS constructed so as to reflect accurately the relative abundance of determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

S Sequence 87 BP; 35 A; 21 C; 16 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7513 CCTGGCTAATTTTTGTATTTTAGGAGATGGGGTTTCACCATGTTGGCCAGACTGGTC 7572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
U3-AUG-1996 (first entry)
Human gene signature HUMGS02944.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
Gell typing; abnormal cell function; ss.
                                                                                                                                                                                                                          - e.g.
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human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                       WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 87;
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Pred. No. 0.63;
0; Mismatches
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cell typing; abnormal cell function; ss.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1996 (first entry)
Human gene signature HUMGS09078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%;
Best Local Similarity 79.8%;
Matches 67; Conservative
                                                                                                                                      11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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                                                                                                                                                                (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
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                                                                                                                         01-JUN-1995.
                                                                                                                                                                                               Matsubara K,
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T26828
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couble-stranded DNA, or its complementary strand or the corresp.

double-stranded DNA, which comprises one of the 7837 "GS" sequences given in 179001-175837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 108 BP; 18 A; 33 C; 28 T;
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A single-stranded DNA (or its complementary strand or the corresp.

A single-stranded DNA (or its complementary strand or the corresp.

Gouble-stranded DNA) which comprises one of the 7837 "GS" sequences

given in T19001-T26837 and which is able to hybridise to part of

Comman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

Comman dof mRNA by using poly(T) as the sole primer. Since the 3'-

untranslated sequence is unique to a particular mRNA species, almost

all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for

Sequence 9? BP; 19 A; 27 C; 20 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20285 GATCTCCTGACCTCATGATCTGCCCACCTCAGCCTCCCAAAGTGCTAGGATCACAGGCAT 20344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.59;
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0; Mismatches
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1 Similarity 77.5%;
69; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
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WPI; 95-206931/27.
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WO9514772-A1.
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Homo sapiens.
                  30-MAR-1999
                                                                                                                                        14-MAY-1998.
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testing polymorphic typing for disease
Claim 1, Page 219; 310pp; English.

X10269-X1237 are human DNA fragments which contain biallelic polymorphic
markers which have been isolated using the primers represented in
X10269-X1237 are human DNA fragments which contain biallelic polymorphic
markers which have been isolated using the primers represented in
X10269-X1237 are human DNA fragments which contain biallelic polymorphic
X10261-X10268 The base occupying the polymorphic stragments can be used in
methods for determining polymorphic forms in an individual for use in
C. Grensles, paternity testing or for phenotypic typing for diseases
cuch as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
hypercholesterolemia, polycystic kidney disease, hereditary
harmorrhagic telanglectasia, familial colonic polyposis, Ehlers-Danlos
Syndrome, osteogenesis imperfecta, acute intermittent porphyria,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25232 GTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAAGCAGATCACTTGAGGT 25291
                                                            7593 GATCTGGCCACCTCGGCCTCCCGAAGTGCTGGGATTACAGGTGTGAGCCATGGCGCCAGA 7652
                                                                                                                                                                                                                                                       30-MAR-1999 (first entry)

Human biallelic polymorphic DNA fragment EST98276a.

Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                  Gaps
                                                                             Gaps
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Madson T. Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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   DB 1; Length 97;
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Pred. No. 0.9;
1; Mismatches 26; Indels
                               23; Indels
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0.2%; Score 57.4; DB 75.3%; Pred. No. 0.78;
                                                                                                                       7653 CCTGGACTTTGTCTTCTGTTTCATCAGTCCTTC 7685
                             0; Mismatches
                                                                                                                                                   61 NCTGTACTAAGTCTTTTTTTTTAAATTTCCTC 93
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ID X12085 standard; DNA; 100
                               70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1997; U20313.
06-NOV-1996; US-030455.
                                                                                                                                                                                                                                                                                                                                   treatment; marker; ss
                 Local Similarity
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WO9820165-A2.
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The Manuacau uniquestic acts as a second of the containing polymorphic forms for use in e.g. forensics, paternity and testing or phenotypic typing for disease

Esting or phenotypic typing for disease

Claim 1. Page 218; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occuping the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in e.g. forensics, paternity testing or forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammagiobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Addrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary cauchimmune diseases, inflammation, cancer, diseases of the nervous cauchimmune diseases, inflammation, cancer, diseases of the nervous of the paracteristics such as a paracteristics.
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                                                                           testing; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                           Human biallelic polymorphic DNA fragment EST98276c.
Polymorphism; biallelic; human; forensic; paternity testing; disease, detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament,
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Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                                                                                                                                                                                                     05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHITPERAD INST BIOMEDICAL RES.
Hudson T. Lander ES, Wang D;
WPI; 98-286974/25.
New isolated nucleic acid segments from the human genome - used for
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Human gene signature HUMGS02180.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
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1; Mismatches
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Best Local Similarity 72.7
Matches 72; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUBA) OKUBO K.
MATSUBARA K. OKUBO K;
WPI; 95-206931/27.
                                                                                                                                                                                              treatment; marker; ss.
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WO9514772-A1.
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PT for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human PT reflects relative abundance of corresp. mRNA in specific human PT rissues

C laim 1; Page 758-759; 2245pp; Japanese.

C A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences could be complementary strand or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared comman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared conversions human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the specific mRNAs. Each library constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be CC determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

So Sequences 103 BP; 22 A; 27 C; 21 G; 31 T;
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Gaps

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Ouery Match 0.2%; Score 57.2; DB 1; Length 103; Best Local Similarity 77.3%; Pred. No. 0.84; Matches 68; Conservative 0; Mismatches 20; Indels

Search completed: June 16, 2000, 12:11:56 Job time: 170027 sec

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FEATURES		ACCESTON VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
AA703692 agglal0.r AA243092 zz525062.s AA250812 zs65605.s B48914 RPCII1-4A12 AA835205 ax64401.s AA835205 ax64401.s AA381369 EST94442 B65160 CIT-HSP-201 AA654562 nt.75f10.s AA65452 nt.75f10.s AA65533 nk42b11.s AA65533 nk42b11.s AA65530 nk42b11.s AA65456 nt.75f10.s AA65456 curff10.s AA65456 nc.75f10.s AA65456 re.75f10.s AA65456 re.75f10.s AA65456 re.75f10.s AA65456 re.75f10.s AA65456 re.75f10.s AA65466 CIT-HSP-2 AA244245 nc.77a1.s AQ240182 CIT-HSP-2 AQ240182 CIT-HSP-2	AQ38682 RPCIII-13 AQ028649 CIT-HSP-2 AQ535244 RPCII-1-3 AC991750 Wt468601.x AT991750 Wt468601.x B17434 34582.TVB C B17434 34582.TVB C B17434 34582.TVB C AQ381369 EST94442 AQ381369 EST94442 AQ381369 EST94442 AQ381369 EST94442 AQ581425 RPCI-11-4 AQ581425 RPCI-11-4 AQ5812925 RPCI-11-4 AQ581211-04048102.x AQ321855 RPCIII-11 AA250812 ZS06805.s AA7700000 tt36810.x AQ321865 RPCIII-11 AA278889 ZQ15604.s AA078003 7H12D08 C AQ386882 RPCIII-13 AA386808 EST99495 AQ076649 CIT-HSP-2 AQ260734 CIT-HSP-2	ALIGNMENTS  p mRNA EST 24-DEC-1997  ne hNT neuron (#937233) Homo saptens cDNA clone  nilar to contains Alu repetitive element;, mRNA  610  Chordata; Craniata; Vertebrata; Mammalia;  Catarrhini; Hominidae; Homo.  T. Lacy,M., Le,N., Lennon,G., Marra,M.,  Schellenberg,K., Steptoe,M., Tan,F.,  Y., Wylie,T., Waterston,R. and Wilson,R.  Project
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N., Lennon,G., Marra,M.,
f., Steptoe,M., Tan,F.,
aterston,R. and Wilson,R.
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Gaps

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Venerations of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)

Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Nedical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 401 838 0200
Fax: 401 838 0200
Fax: 501 838 020
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY 10321 TAGAGACGGGGTTTCACCATGTTGGCCAGGCTGTCTCAAACTCCTGACCTCAGGTGATC 10380
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/note="Vector: pBACe3.65 Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
1 28 c 30 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B48914 103 bp DNA GSS 08-APR-1999 RPCIII-4A12.7P RPCI-11-4A12, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TAGAGACGGGGTTTCACCATGTTGGCCAGGCGGTCTCAAACTCTTGACCTCAGGGGATC 61
                                                                                                                                                                                                                                                                                                                                            Query Match 0.3%; Score 90.4; DB 30; Length 106; Best Local Similarity 94.0%; Pred. No. 0.4; Matches 94; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .103
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                            NCICGAP http://www.ncbl.nlm.nih.gov/ncicgap.
NCICGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
On Sep 12, 1996 this sequence version replaced gi:1407356.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royality-free through LLNL; contact the IMAGE Consortium (info@lange.llnl.gov) for further information.
Insert Length: 537 Std Error: 0.00
Seq primer: -41m3 wd. ET from Amersham
High quality sequence stop: 87.
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AA250812
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
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/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
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Pred. No. 0.31;
0; Mismatches 11;
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/db_xref="taxon:9606"
Location/Qualifiers
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AA250812.1 GI:1885774
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Best Local Similarity 89.9%
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
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                                                                                                                                                                                                                                                                                                                      AA835205 101 bp mRNA EST 23-FEB-1998 ak64h01.s1 Barstead pancreas HPLRB1 Homo sapiens CDNA clone IMAGE:1412689 3' similar to contains Alu repetitive element; contains element KER repetitive element; , mRNA sequence. AA835205.1 GI:2908933
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                                                                                    20236 TGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTAGCCGGGATGGTCTCGATCTCCTGAC 20295
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Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washb-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -40ml3 frvd. ET from Amersham.
Location/Qualifiers
                                              Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Wilson RK
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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  Length 103;
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/clone_lib="Barstead pancreas HPLRB1"
                                                                                                                                                                                               43 CTCGTGATCCGCCCCCCCTCGCCTCCCAAAGTGCTGGGCTTAC 1
  DB 84;
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0.3%; Score 88.6; DB
11.3%; Pred. No. 0.63;
ve 0; Mismatches
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/lab_host="DH108"
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/db_xref="taxon:9606"
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ilarity 92.1%;
Conservative (
                    91.3%;
                                          94; Conservative
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Rashington University Genome Sequencing Center
Clone distribution: NCI-CGRP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                           nc07a04.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1007406 similar to contains Alu repetitive element;, mRNA sequence. AA244245
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
On Jan 24, 1995 this sequence version replaced g1:634306.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88.2; DB 30; Length 110;
Pred. No. 0.68;
0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -41ml3 fwd. ET from Amersham
GCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by David Krizman."
26 c 28 g 38 t
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/clone_lib="NCI_CGAP_Prl"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .110
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local
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AA244245/C
                                                                                                                                                                        DEFINITION
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                     61
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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21-JUN-1998

RESULT 7 AA381369/c DEFINITION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

ACCESSION VERSION

```
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA654562 102 bp mRNA EST 04-NOV-1997 nt75f10.s1 NCI_GGAP_PT3 Homo sapiens CDNA clone IMAGE:1204363 aimilar to contains Alu repetitive element; contains element MER22 repetitive element; , mRNA sequence.
                                                                                                                                                                                                                                Eutherla; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Goolden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simor, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25365 TGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAAGAATTGCTTGAA 25424
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                                             B65160 108 bp DNA GSS 21-JUN-1998
CIT-HSP-2017G2.TRB CIT-HSP Homo sapiens genomic clone 2017G2,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87.8; DB 84; Length 108;
Pred. No. 0.76;
0; Mismatches 12; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Other_GSSs: CIT-HSP-2017G2.TFB
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7043860"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="2017G2"
/clone_lib="CIT-HSP"
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Best Local Similarity 88.8%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                  B65160.1 GI:2639138
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                                                                          DEFINITION
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                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                   AUTHORS
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RESULT
B65160
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Eutheria; Frimates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

8 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Blatke,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Flizgerald,L.M., Flizhudh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm.C.L., Hanna,M.C., Hachlom,E., Hinkle,P.S.J. Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,J.L., Naudek,D.T., Palligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shriey,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Lii,Y., Dimke,D.P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Baymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon, R.P., Rosen,C.A., Haseltine,W.A., Fields,C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
                  AA381369 101 bp mRNA EST 21-APR-1997
EST94442 Activated T-cells I Homo sapiens CDNA 5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oy 13186 AAAATTAGCTGGGTGTGGTGGCGGGCACCTGTAATCCCAGCTAATCAGGAGACTGAGGCA 13245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 12, 1996 this sequence version replaced gi:1407448.
Other_ESTs: THC170052
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
TEL: 3018699056
Fax: 3018699423
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                                                                  EST containing Alu repeat, mRNA sequence.
AA381369.1 GI:2033689
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/db_xref-"taxon:9666"
/clone_lib-"Activated T-cells I"
/cell_type-T-lymphocyte"
/dev_stage="adult"
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0; Mismatches
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Matches 92; Conserv
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MEDLINE COMMENT

JOURNAL

TITLE

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Gaps

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Homo sapiens

human.

41 GGANAATTGCTTGAACCCAGGAGGCGGAGGTTGCAATGAGC 1

BASE COUNT

FEATURES

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Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
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Brail: Robert_Strausberg@nlh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA565533 107 bp mRNA EST 08-SEP-1997 nk42b11.s1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1016157 3' similar to contains Alu repetitive element; , mRNA sequence.
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1. (basea: 10.7)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1393355.
  Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20112 GGAATGCAGTGGCACAATCTCGGCTCACTGCAACCTCCGGCTCCCGGATTCACGCCATTC 20171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 36 c 25 g 22 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Feb 19, 1999 this sequence version replaced gi:4146076.
On Feb 19, 1999 this sequence version replaced gi:4146076.
On Feb 19, 1999 this sequence version replaced gi:4146076.
Onter_GSS: RPCI-II-1451AIS.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 103;
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GDB:7672814"
/db_xref="taxon:9606"
/clone="RPCI-11-451A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11"
/sex="Male"
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AA565533.1 GI:2337172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // Arabetor: pawplo; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells

5,000-10,000 microdissected cells

histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMPlo by the DGC-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                                                                                                                                          Onpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393451.
On Sep 12, 1996 this sequence version replaced gi:1393451.
Contact: Robert Strausberg, Ph.D.
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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RPCI-11-451A15.TJ RPCI-11 Homo sapiens genomic clone
RPCI-11-451A15, genomic survey sequence.
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                  Eutheria; Primates; Catarrhini; Hominidae; Homo (bases 1 to 102)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
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0; Mismatches
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1204363"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David Krizman.
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Matches 92; Conservative
                                                                                                                             Tumor Gene Index
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                                               REFERENCE
AUTHORS
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Gaps

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Unpublished (1998)

Unpublished (1998)

Unpublished (1998)

Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 3010 888 0200
Fax: 301 888 0200
Fax: 301 888 0200
Fax: 301 888 from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://Pacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                     /note="Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 110)

Adams; M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20147 TCCGCCTCCCGGATTCACGCCATTCTCCTGCCTCAACCTCCCGAGTAGCTGGGACCACACA 20206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ003188 110 bp DNA GSS 14-APR-1999 RPCI11-1D10.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1D10,
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Pred. No. 1.1;
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                                                                            /db_xref="taxon:9606"
/clone="IMAGE:1373364"
/clone_lib="NCI_CGAP_Ov2"
                                                   /organism="Homo sapiens"
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/db_xref="GDB:7500081"
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                                                                                                                                                                              /tissue_type="ovary"
/lab_host="DH10B"
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Location/Qualifiers
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                                                                                                                                                           /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.3%;
Best Local Similarity 89.4%;
Matches 93; Conservative
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AQ003188
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1016157"
/clone_lib="NCI_CGAP_GC2"
/tissue_type="germ cell tumor"
/tab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr. Bulk
germ cell tumor. 5' adaptor sequence: 5' GAATTCGGCACGAG 3'
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'
Average insert size: 1.2 kb."
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                                           DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1899815.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 TGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATCACTTGAACCT 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 25428 AGGAGGGGGGGGTTGCAGTGAGCCGAAATCGCGCCACTGCACTCCAG 25474
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                           cDNA Library Arraying: Greg Lennon, Ph.D.
                                                                                                                                                                              Insert Length: 1661 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
1. 107
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.1;
0; Mismatches
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Best Local Similarity 87.9%;
Matches 94; Conservative
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KEYWORDS
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Indels

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Length 102;

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Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleteredejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
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1 (bases 1 to 103)
2 Sabo.S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                        10324 AGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATCCAC 10383
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/cell_type="Lymphocytes"
/notel='Veyte="Lymphocytes"
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/notel='Veyte="Lymphocytes"
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RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
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                                                                                                                                                                                                                                                                              1 AGACGAGGTTTCACCATGTTGGCCAGTCTGGTCTCAAACTCCGGACCTCAGGTAATCCGC 60
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Contact: Shaying Jahoo, William Nierman, Mark Adams
Contact: Shaying Jahoo, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
912 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                           Qy 10384 CTGCCTCGGCCTCCCAAATGCTGAGATTACAGGTGTGAGCC 10425
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 86; DB 36;
Pred. No. 1.2;
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89.3%; Pred. No. 1.4;
ilve 0; Mismatches
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/db_xref="GDB:7621533"
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/clone="RPCI-11-317H22"
/clone_lib="RPCI-11"
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                                                                                                       0.3%;
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Matches 92;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                              Gaps
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393451.
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                         Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TGACCTCATGATCCACCTGCCGCAGCCTCCCAAAGTGCTGGGATTACAG 110
                                                                                                                                                                                                  Score 86.6; DB 94; Length:
Pred. No. 1;
0; Mismatches 14; Indels
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Location/Qualiflers
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/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
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/lab_host="DH10B"
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                                                                 26 g
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87.2%;
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Best Local Similarity
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COMPOURT: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
US-08-340-426D-92
US-08-450-73C-92
US-08-340-426D-91
US-08-340-426D-91
US-08-450-673C-91
US-08-450-673C-91
US-08-450-673C-91
US-08-450-673C-91
US-08-340-426D-57
US-08-340-426D-69
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-69
US-08-481-658B-66
US-08-481-658B-66
US-08-477-504A-66
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Pred. No. 2.8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Pro
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STRRET: 6 Mariposa Court
CITY: Tiburon
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 65, Application US/08481658B; Patent No. 5955075; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Laucer, Leona L. REGISTRATION NUMBER: 3
   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: USA
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Best Local Similarity
   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94920
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US-08-481-658B-65
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 RESULT
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(without alignments)
10124.339 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/Packfiles1.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-485-855A-65
US-08-485-855B-65
US-08-481-658B-65
US-08-481-658B-65
US-08-486-756A-65
US-08-486-756A-65
US-08-486-756A-65
US-08-457-79-65
US-08-787-739-65
US-08-787-730-70
US-08-787-79-70
US-08-450-673C-70
US-08-450-673C-70
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US-08-454-557C-69
US-08-340-426D-69
US-08-450-673C-69
US-08-454-557C-92
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US-08-340-426D-91
US-08-450-673C-91
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 110
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                                                                  2 ITITIACATCITIAGTAGAGACAGGGTITCACCATATITGGCCAGGCTGCTCTCAAACTCC 61
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SOFTWARE: PACEDIL RELEASE #1.0, Version #1.30 (EPO);
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
FRICR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:

NAME: LAUGHT. LB-GONA L.

REGISTRATION NUMBER: D-0021.3D
TELECHONE: 415-435-0334
TELECHONE: 415-435-0334
TELECHONE: 415-435-0727
INFORMATION FOR SED ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANBENESS: single
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  0; Mismatches 16; Indels
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                                                                                                                              Qy 19497 TGACCTCATGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGAT 19540
                                                                                                                                                     0.3%; Score 78.4; DB 4;
84.6%; Pred. No. 2.8e-08;
tive 0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: M Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             US-08-477-504A-65; Sequence 65, Application US/08477504A; Sequence 65, Application US/08477504A; Patent No. 5972353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 84.65
Matches 88; Conservative
  88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6 Mariposa
CITY: Tiburon
STATE: California
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US-08-477-504A-65
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  Matches
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QY 19437 TTTTTGTATTTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTCCAACTCC 19496
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Pred. No. 2.8e-08;
0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Maliposa Court
                                                               APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STRET: 6 Mariposa Court
CITY: Tiburon
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/486,756A FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-0021.3C
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-485-8628-65
; Sequence 65, Application US/084858628
; Patent No. 5989838
; GENERAL INFORMATION:
Sequence 65, Application US/08486756A Patent No. 5981711 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.3%;
                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.3°
Best Local Similarity 84.6°
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                      ZIP: 94920
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US-08-486-756A-65
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RESULT

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
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STREET: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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STATE: California
COUNTRY: USA
ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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US-08-481-658B-65/c
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US-08-787-739-65
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                                                                COMPUTE READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: TBM PC compatible
COMPOTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/477,504
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTONEY/AGENT INFORMATION:
NAME: LAUGET, LEONA LOS 08/260,13D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY 19497 TGACCTCATGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGAT 19540
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TGACCTTGTGATCCACCAGCCTCGGCCTCCCAAAGTGCTGGGAT 105
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Sequence 65, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ 1D NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
California
                          USA
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Qy 19437 TTTTTGTATTTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTCCAACTCC 19496
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84.6%; Pred. No. 2.8e-08;
tive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy 19497 TGACCTCATGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGGAT 19540
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Patent No. 5955075
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE AND DATE: 0/-007-1993
PRICE AND DATE: 0/-007-1993
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-007-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-007-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-007-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-007-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAUGHEY, LEGORA L.
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
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Qy 13084 ATACCAGCACTTTGGGAGGCCGATGTGGGTGGATCACCTGAGGTCAGGAGTTTGAGACCA 13143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY 13144 GACTGGCCAACATGGTGAAACCTCATCTTGTAAAAATACAAAA 13189
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/486,756A
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 GCCTGGCCAATATGGTGAAACCCTGTCTACTACTAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zavada, Jan
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mailposa Court
                                                            D-0021.3D
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APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 65, Application US/08486756A; Patent No. 5981711
; GENERAL INFORMATION:
                                REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET UNMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-435-0727 INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TYPE: nucleic acid
STRANDEDNESS: single
            Lauder, Leona L.
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STATE: California
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US-08-486-756A-65/c
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US-08-477-504A-65
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84.0%; Pred. No. 5e-06;
tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 13144 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 13189
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE:
CLASSIFICATION: 424
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GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastcrekova, Silvia
APPLICANT: Pastcrekova, Silvia
APPLICANT: Pastcrekova, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Leander
STREET: 6 Mariposa Court
CITY: Tiburon
STRATE: California
COUNTRY: USA
                                                                                                                                                                      CLASSIFICATION: 474
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    D-0021.3E
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
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Best Local Similarity 84.08
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94920
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US-08-481-658B-65
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13084 ATACCAGCACTTTGGGAGCCCGATGTGGGTGGATCACCTGAGGTCAGGAGTTTGAGACCA 13143
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 24-JAN-1997
PRIOR APPLICATION NUMBER: 28-JAN-1997
PRIOR APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                               Qy 13144 GACTGCCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 13189
                                                                                                                        us-08-787-739-65/c
; Sequence 65, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION;
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE AND LALLS.
PRICE AND LALLS.
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-70N-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-70N-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-70N-1995
PRICE APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-70N-1995
PRICE APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-70N-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lauder, Leona L.
REGISTRATICN NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-981-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS: LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-08-787-739-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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                                                                                                                                                                                                                                       13084 ATACCAGCACTTTGGGAGGCCGATGTGGGTGGATCACCTGAGGTCAGGAGTTTGAGACCA 13143
                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                             105 ATCCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCAC--AAGGTCAGGAGTTTGAGAGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 68; DB 4; Length 105; 84.0%; Pred. No. 5e-06; Live 0; Mismatches 15; Indels
                                                                                                                                       Score 68; DB 4; Length 105;
Pred. No. 5e-06;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                  QY 13144 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAA 13189
                                                                                                                                                                                                                                                                                                                                                             47 GCCTGGCCAATATGGTGAAACCCTGTCTACTACTAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FACENCAL INCORNATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREFT: 6 Mariposa Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lauder, Leona L.
REGISTRATION UNDBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-485-862B-65/c; Sequence 65, Application US/08485862B; Patent No. 5989838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO; ANTI-SENSE: NO US-08-486-7568-65
                                                                                                                                         Query Match 0.2%;
Best Local Similarity 84.0%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.2
Best Local Similarity 84.0
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6 Mariposa
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>8</u>
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US-08-485-862B-65
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; TOPOLOGY:
US-08-340-426D-70
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Patent No. 5830670
GENERAL INFORMATION:
APPLICANT de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY 19422 ACCAAGCCCGGCTAATTTTGTATTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGG 19481
                                                                            Qy 13084 ATACCAGCACTTTGGGAGGCCGATGTGGGTGGATCACCTGAGGTCAGGAGTTTGAGACCA 13143
                                        Gaps
                                                                                                Gaps
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Score 68; DB 5; Length 105;
Pred. No. 5e-06;
                                                                                                                                                    QY 13144 GACTGGCCAACATGGTGAAACCTCATCTCTAGTAAAAATACAAAAA 13189
                                      15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  ...urESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFTCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig Steven R.
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-2540
TELEPHONE CHARACTERISTICS:
                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 19482 CTGGTCTCCAACTCCTGA 19499
0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
                                      89; Conservative
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-454-557C-70
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  Query Match
                                      Matches
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US-08-450-673C-70
Sequence 70, Application US/08450673C
Sequence 70, Sp4888
Fatent No. 594888
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19422 ACCAAGCCCGGCTAATTTTGTAGTAAAGACGGGGTTTCACCATGTTGGTCAGG 19481
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                                                                                                                                                                      ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIND APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.2%; Score 60.4; DB 4; Best Local Similarity 85.9%; Pred. No. 0.00019; Matches 67; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0609.3840002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY 19482 CTGGTCTCCAACTCCTGA 19499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTGGTGTCGAACTCCTGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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PCT-US95-17111A-70
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US-08-454-557C-70
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                                                                                                                                                                                                                                Matches
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PCT-US95-17111A-70

Sequence 70, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS: 221
CORRESPONDENCE ADDRESS: 321
CORRESPONDENCE ADDRESS: 321
CORRESPONDENCE ADDRESS: 321
CORRESPONDENCE ADDRESS: 321
COUNTRY: Washington
STATE D.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER: Eloppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
FIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 A PARCECCEAGCTARATATTGTATTTTAGTAGAGATGGGGTTTCTCCATGTTCATCAGG 60
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85.9%; Pred. No. 0.00019;
tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70: SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                   APPLICATION DAIR

FILING DATE: 30-MAY-1995
FILING DATE: 30-MAY-1995
GTASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LUCATION: Steven R.
REGISTRATION NUMBER: 36,203
REFRENCE/DOCKET NUMBER: 36,203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-260
TELEFAK: (202) 371-260
INFORMATION FOR SED ID NO: 70: SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANBEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILLING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY 19482 CTGGTCTCCAACTCCTGA 19499
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Best Local Similarity 85.99
Matches 67; Conservative
CURRENT APPLICATION DATA:
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US-08-450-673C-70
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QY 19422 ACCAAGCCGGGTAATTTTGTATTTTAGTAAAGACGGGGTTTCACCATGTTGGTCAGG 19481
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                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY 1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.8; DB 3;
Pred. No. 0.00042;
0; Mismatches 12;
0.2%; Score 60.4; DB 6;
85.9%; Pred. No. 0.00019;
ative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0609.3840003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,203
REFERENCE/COCKET NUMBER: 0609.
TELECOMMUNICATION INFORMATION:
TELEFRAM: (202) 371-2600
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                Qy 19482 CTGGTCTCCAACTCCTGA 19499
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Best Local Similarity 84.6%;
Matches 66; Conservative
                                                                                                                                                     61 CTGGTGTCGAACTCCTGA 78
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                                 67; Conservative
 Query Match
Best Local Similarity
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Search completed: June 16, 2000, 08:52:43 Job time: 158293 sec

us-08-852-495c-1\_copy\_112000\_141000.rni

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9.59
                                                                          June 16, 2000, 08:46:10; Search time 17973.3 Seconds (without alignments) -1569.657 Million cell updates/sec
                                                                                                                                US-08-852-495C-1_COPY_140000_169000
29001
1 CCTCCAATCCCATATGCAC......TGTTATCACAGAAAGTTACC 29001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               882769 seqs, -486395729 residues
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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1: gb_bal:*

2: gb_ba2:*

3: gb_ov:*

4: gb_ov:*

5: gb_pat:*

6: gb_ph:*

7: gb_pl:*

10: gb_pr2:*

11: gb_pr2:*

11: gb_pr3:*

12: gb_un:*

13: gb_un:*

14: gb_sy:*

15: gb_un:*

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17: em_fun:*

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18: em_lum2:*
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em_un:*
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gb_htg1:*
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em_hum4:*
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9b_htg3:*
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9b_htg5:*
9b_htg6:*
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Maximum DB seq length: 110
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Sequence:
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em_htg1:*
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gb_htg9:*
gb_htg9:*
gb_htg1:*
gb_htg11:*
gb_htg11:*
gb_htg11:*
gb_htg7:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Searched:

Run on:

		U67803 Human small	X05250 Human LDL-r	Human c	M87899 Human carci	0 Human		O	U67808 Human small	X57789 Human seque	Human 1		X57789 Human segue	Нитап	Human	Human	L30244 Human STS U	S79560 HRX (intron	I			Human	luman 1	U67807 Human small	Human	Ŧ.		G32655 A009L30 Hum	M141/8 Human Low d	U6/806 Human Small	130134 Human Hebez	Human	Human f	X05249 Human LDL-r	X05251 Human LDL-r		G43535 WIAF-2393-S	D45223 Human GALNS	X66361 H.sapiens m	X91545 H.sapiens D	L31299 Human STS U	K03555 Human low d	I	-	G32906 A009W09 Hum
		HSU67803	HSI,DI,RN2	HUMALCE162	HUMALCE272	HSLDLRN2	HSU67804	HUMALCE221	HSU67808	HS8IC8R	HUMLDLRA1	HUMALCE162	HS8IC8R	HSLDLRD1	HSLDLRD2	HSU67807	HUMUT8164A	879560	HUMALCE221	HSLDL112	643535	HUMALCE43	HUMLDLRA2	HSU67807	HUMLDLRDJ	HUMLDLRA2	HUMUT931A	G32655	HUMLDLRAI	HSU6/806	HUMULDUSMS HUMUTABOOSB	HIMIT 8002B	HUMLDLRDJ	HSLDLRD1	HSLDLRD2	HUMLDLRM	G43535	HUMGALNSA	HSSTHPKIB	HSLAS27	HUMUT931A	HUMLDLRFL	879560	AR051521	G32906
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	Query Match Length DB	108	108	107	104	108	108	103	108	103	97	107	103	108	108	110	91	101	103	108	108	110	97	110	97	97	100	105	76,	107	100	2.5	97	108	108	90	108	100	95	100	100	90	101	84	102
оP	Query Match	0.3	0.3	0.3	0.3		0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	٠	0.3		0.5		0.3		0.5		0.5				7.0	٠	•		9.5		•		٠	٠	0.5		0.5	•	0.5	0.5	0.2
	Score	85.8	85.2	80.6	79.2	77.6	77.8	16	76.2	75.4	75	75	74.4	4	74.6	74.4		72.4	72.4	72.4	72.6	ς,	72	;	71.4	۲,	70.8	71	70.7	0 0 0 0 0 0	4.00	4.4	68.6	9.89	æ	7	^	67.2	9	99	99	5	65.8	65.4	S
	Result No.	1	2	m	4	0	9	7	89	6	c 10	c 11	c 12		14	15	16		c 18			21		c 23			c 26		28	67.6	30	32		34	c 35	36	37	38	c 39	40	41	c 45		C 44	c 45

ALIGNMENTS

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Query Match
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HUMALCE272
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                                                                                                                                                                                                                                                                                                                 Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Direct Submission
Submitsed (22-A06) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24035 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAA 24094
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
                                  01-AUG-1997
                                                                                                                                                                                                              Shaikh,T.H., Roy,A.M., Klm,J., Batzer,M.A. and Deininger,P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.3%; Score 85.8; DB 11; Length 108; 92.8%; Pred. No. 0.00045; Live 0; Mismatches 7; Indels 0;
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
1. Catton/Qualifiers
1. .108
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                             HSU67803 108 bp RNA
Human small cytoplasmic Alu transcript.
U67803
U67803.1 GI:2289917
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97415756
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TscAlu2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
/rpt_type=dispersed
39 c 30 g
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Matches 90; Conserv
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 107)

Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.

Alu RNA transcriptis in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                       24141 AAAAATTAGCCAGGCATGGTAGCACATGCCTGTAATCCCAGCTACTACAGAGGCTGAGGC 24200
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                                                                                                                                                                                                                                                                                               3 AAAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGC 62
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Human carcinoma cell-derived Alu RNA transcript, clone CE272.
M87899
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
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                                                                                                                                                                        Length 108;
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Pred. No. 0.00055;
0; Mismatches 13;
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Pred. No. 0.0028;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
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/sex="male"
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Best Local Similarity 86.4
Matches 89; Conservative
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01-AUG-1997

PRI

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Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Shaikh,T.H., Kim,J., Batzer,M.A. and Deininger,P.L.
Submission
Submission
Submitted (22-40G-1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
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1 (bases 1 to 103)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Shaikh, T. H., Roy, A. M., Kim, J., Batzer, M.A. and Deininger, P.L. CDNAs derived from primary and small cytoplasmic Alu (scAlu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 0.3%; Score 77.8; DB 11; Length 108; 1 Similarity 87.6%; Pred. No. 0.0074; 85; Conservative 0; Mismatches 12; Indels 0
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Homo sapiens male embryo carcinoma cDNA to other RNA
Homo sapiens
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                                                           HSUG7804 108 bp RNA
Human small cytoplasmic Alu transcript.
UG7804.1 GI:2289918
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="TscAlu3"
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/rpt_type=dispersed
38 c 26 g
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/note="scAlu"
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Frimates; Catarrhid; Hominidae; Homo.
I (bases 1 to 108)
Horsthemke,B., Beisiegel,U., Dunning,A., Havinga,J.R.,
Williamson,R. and Humphries,S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
Eur. J. Blochem. 164 (1), 77-81 (1987)
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          Interact, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of
post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
1. 104
/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
/ cell.line="Nyera2D1"
/ dev_stage="embryo"
/ sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 108 CTCGGCTCACTGCAACCTCTGCCTCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCG 49
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Data kindly reviewed (07-DEC-1987) by HUMPHRIES
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Pred. No. 0.0046;
0; Mismatches 1:
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/db_xref="taxon:9606"
1. .108
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26 c 37 g 1
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1 Similarity 87.0%;
87; Conservative
  1 (bases 1 to 104)
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                                                                                                                          Qy 24167 TGCCTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGGGAATTGCTTGAACCCGGGAGGT 24226
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
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                                                                 Score 76; DB 9; Length 103;
Pred. No. 0.014;
0; Mismatches 15; Indels
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Direct Submission
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Human sequence tagged site BICBR DNA from 19q13.
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Human small cytoplasmic Alu transcript.
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/db_xref="taxon:9606"
/clone="TscAlu7"
1. .108
/tissue_type="carcinoma"
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/rpt_type=dispersed
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Best Local Similarity 86.6%;
Matches 84; Conservative (
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Matches 85; Conservative
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Analysis of the LDL-receptor gene of a patient with familial hypercholesterolemia (FH) revealed the deletion of exon 5 resulting from a homologous recombination between repetitive Alu sequences of
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           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Aldridge,F.L.

Direct Submission

Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals, Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK

2 (bases 1 to 103)

2 (bases 1 to 103)

Butler,R. Riley,J.H., Ogilvie,D.J., Anand,R., Buxton,J., Davies,J., Johnson,K. and Markham,A.F.

Two sequence-tagged sites defining the ends of a 380 kb YAC clone
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Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97)
1 (bases 1 to 97)
1 (bases 1 to 97)
2 (Goldstein, J.L. and Russell, D.W.
Deletion of exon encoding cysteine-rich repeat of low density
lipoprotein receptor alters its binding specificity in a subject
With familial hypercholesterolemia
97008518
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91367697
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Db 61 ATCCACCTCGACCTCCCAAAGTGCNGAAAT 94
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/clone="8IC8"
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low density lipoprotein receptor-1.
1 of 2
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/db_xref="taxon:9606"
/map="19p13.3"
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/db_xref="taxon:9606"
/chromosome="19q13"
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Location/Qualiflers
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Homo sapiens
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BASE COUNT

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*Source: hypercholesterol aemia
See X05248 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.
Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in the low-density-lipoprotein-receptor gene. A possible mechanism for the defect in a patient with familial hypercholesterolaemia Eur. J. Blochem. 164 (1), 77-81 (1987)
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
1. .108
                                                          Submitted (12-FEB-1991) F.L. Aldridge, ICI Pharmaceuticals, Alderley Park, Macclesfield, Cheshire, SK10 4TG, UK
2 (bases 1 to 103)
Butler,R., Riley,J.H., Ogllvie,D.J., Anand,R., Buxton,J.,
Davies,J., Johnson,K. and Markham,A.F.
Two sequence-tagged sites defining the ends of a 380 kb YAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSLDLRD1 108 bp DNA PRI 20-MAY-1992 Human LDL-receptor mutated gene with intron 12 deletion junction.
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m c} 20 9~28~{
m t}
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Primartes; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108)
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
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Pred. No. 0.025;
Triffic 17; Indels
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/clone="8IC8"
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    103
/organism="Homo sapiens"
/db_xref="taxon:9606"

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1 Similarity 83.2%;
84; Conservative
  1 (bases 1 to 103)
Aldridge, F.L.
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X05249.1 GI:34335
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HSLDLRD1/c
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1 (bases 1 to 107)
Sinnett, D., Richer, C., Deragon, J.-M. and Labuda, D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                        16558 ITTITIGAGATGGAGTCTTACTCTGTCGCTCAAGCTGGAGTGCAGTGGCACAATCTCAGC 16617
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                                                                                                                                                                                                                    Gaps
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Human carcinoma cell-derived Alu RNA transcript, clone CE162.
M87924
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'note-"LDL-receptor intron D; G00-119-362"
                                                                                                                                                                  Query Match 0.3%; Score 75; DB 9; Length 97; Best Local Similarity 89.0%; Pred. No. 0.02; Matches 81; Conservative 0; Mismatches 10; Indels
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                                                             sequence"
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/db_xref="taxon:9606"
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/sex="male"
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                  42. 72
/gene="LDLR"
/note="deletion ta
a 34 c 26 g
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STS; myotonic dystrophy.
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FEATURES

BASE COUNT ORIGIN

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RESULT 12

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Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Horsthemke, B., Beisiegel, U., Dunning, A., Havinga, J.R.,
Hillamson, R. and Humphries, S.
Unequal crossing-over between two alu-repetitive DNA sequences in
the low-density-lipoprotein-receptor gene. A possible mechanism for
the defect in a patient with familial hypercholesterolaemia
Bur J. Blochem. 164 (1), 77-81 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See X05250 for corresponding normal gene sequence
In the defective LDL-receptor gene the deletion ocurred between two
alu-repetitive sequences, that are in the same direction, the
deletion eliminates exons 13 and 14 and changes the reading frame
of the resulting spliced mRNA.

Data kindly reviewed (07-DEC-1987) by HUMPHRIES S.
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/db_xref="taxon:9606"
/cell_type="blood leukocytes from a patient with familial"
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                                                                                                                                                                                                                                                                                                                         HSLDLRD2 108 bp DNA PRI 20-MAY-1992 Manan LDL-receptor mutated gene with intron 14 deletion junction. X05251 X05251. GI:34336 Alu repetitive sequence; low density lipoprotein receptor.
                                                                                                            24141 AAAAATTAGCCAGGCATGGTAGCACATGCCTGTAATCCCAGCTACTCAAGAGCTGAGGC 24200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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                                    Length 108;
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                                  0.3%; Score 74.6; DB 10;
81.9%; Pred. No. 0.023;
tive 0; Mismatches 19;
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Human small cytoplasmic Alu transcript.
U67807
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Matches 86; Conservative
                                                                          Conservative
                                  Query Match
Best Local Similarity
Matches 86; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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Shaikh, T.H., Kim, J., Batzer, M.A. and Deininger, P.L.
Direct Submission
Submitted (2.1996) Human Genetics and Molecular Biology, The
Children's Hospital of Philadelphia, 1004F Abramson Research
Center, 34th and Civic Center Blvd., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QY 13530 GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCGGATCACTTGAAGCCAGGAGTTC 13589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
                                                                                      Shaikh, T.H., Roy, A.M., Kim, J., Batzer, M.A. and Deininger, P.L. cDNAs derived from primary and small cytoplasmic Alu (scAlu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.3%; Score 74.4; DB 11; Length 110;
84.0%; Pred. No. 0.025;
tive 0; Mismatches 16; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcripts
J. Mol. Biol. 271 (2), 222-234 (1997)
97415756
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                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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/rpt_type=dispersed
39 c 24 g
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June 16, 2000, 12:11:56 ; Search time 581.7 Seconds (without alignments) 12473.475 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                            OM nucleic - nucleic search, using sw model
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US-08-852-495C-1\_COPY\_140000\_169000 29001 1 CCCTCCAATCCCATATGCAC......TGTTATCACAGAAAGTTACC 29001 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapox 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

433070 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 10 Maximum DB seq length: 110

Post-processing: Minimum Match 0% Listing first 45 summaries

N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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SUMMAKIES																																				
SOMM		a	T25009	X12095	T24892	X12095	X12087	X12085	T24892	x12086	T25854	T20927	T26828	T26213	T26828	T25009	029016	T22572	T20927	T26213	T24259	T21566	T21566	T26728	X12087	X12085	X12086	T20931	T23131	T23895	T26288	T25854	T25052	T22572	T24259	029016
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		Length	108	108	100	108	100	100	100	100	91	103	108	103	108	108	69	93	103	103	93	87	87	97	100	100	100	66	95	109	110	91	92	93	93	69
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		Score	80.4	73.2	68.8	68.4	63.4	63.4	62.4	62.2	o	61.2	61	9.09	60.4	59.4	58.4	57.4	57.6	56.2	55.8	55.2	55.2	55.2	55.4	55.4	55.4	54.8	10	m	53.6	53	23	52.6	52.6	25
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## ALIGNMENTS

RESULT

105	10001
1	T25009 standard; cDNA to mRNA; 108 BP.
AC	
DI	966
DE	Human gene signature HUMGS07131.
KW	Gene signature; messenger RNA; mRNA; relative abundance; frequency;
ΚW	human; cloning; mapping; non-biased library; diagnosis; detection;
ΚW	cell typing; abnormal cell function; ss.
os	Homo sapiens.
PN	WO9514772-A1.
PD	01-JUN-1995.
PF	11-NOV-1994; J01916.
PR	12-NOV-1993; JP-355504.
PA	(MATS/) MATSUBARA K.
PA	
PI	Matsubara K, Okubo K;
DR	WPI; 95-206931/27.
PT	ignatures in
PŢ	
PT	reflects relative abundance of corresp. mRNA in specific human
PT	tissues
PS	Claim 1; Page 1748; 2245pp; Japanese.
ပ္ပ	A single-stranded DNA (or its complementary strand or the corresp.
ပ္ပ	double-stranded DNA) which comprises one of the 7837 "GS" sequences
ပ္ပ	given in T19001-T26837 and which is able to hybridise to part of
ပ္ပ	human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
ပ္ပ	sequences were obtained from 3'-directed cDNA libraries prepared
ပ္ပ	from various human tissues; synthesis of cDNA was initiated from the
ပ္ပ	3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
ខ្ល	untranslated sequence is unique to a particular mRNA species, almost
ນ	all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
ပ္ပ	is constructed so as to reflect accurately the relative abundance of
ပ္ပ	different mRNAs in the particular tissue from which it was derived.
႘	The appearance frequency of a given GS in a cDNA library can be
ပ္ပ	determined (esp. using primers and probes derived from the GS
ပ္ပ	sequences) as a means of diagnosing abnormal cell function or for
ပ္ပ	recognising different cell types.
δS	Sequence 103 BP; 34 A; 31 C; 26 G; 15 T;
J	Query Match 0.3%; Score 80.4; DB 1; Length 108;
ш	cal Similarity 83.3%; Pred. No. 0.004;
24	Matches 90; Conservative 0; Mismatches 18; Indels 0; Gaps
Q	7698 ITTITITITITITITITGAGACAAGGTCTTGCTCTGTCACTTAGGCTGGAATTCAGTG 775
Ę	OF CHORONERACORDECACECACECECECECECECECECECECECEECEECEECE

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108 TTTGNTGTTGTTGTTTTCAACAGGGTCTTGCTCTGTCACTCAGGCTGGAATNCAGTG 49 ŏ Ор

RESULT 2 X12095/c ID X12095 standard; DNA; 108 BP. g

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                               Human biallelic polymorphic DNA fragment TIGR-A003M18a. Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 CTATAATCCCAGCACTTTTGGGAGGCCAAGGCAGACGGATCACTTGAAGTCAGGAGTTCG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying gene signatures in 3'-directed human cDNA library - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA, mRNA, relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY 13591 AGACCAGCCTGCCCAACATGGCAAAACCCTGGCTCTACCAAAAATACA 13638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 AGACCATCCTGGCCAACAYAGGAAAACCTCATACAAAAAAGACA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73.2; DB Pred. No. 0.037; 1; Mismatches
                                                                                                                                                                      14-MAX-1998.
05-NOV-1997; U20313.
06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T24892 standard; cDNA to mRNA; 100 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1996 (first entry)
Human gene signature HUMGS06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such diseases.
                                                                                                                                                                                                                                                 Hudson T, Lander ES, Wang D; WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%;
                   (first entry)
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Best Local Similarity 85.2
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OKUB/) OKUBO K.
Matsubara K, Okubo K;
WPI; 95-206931/27.
                                                                                                                   treatment; marker; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prophylaxis of
                                                                                                                                                  WO9820165-A2.
                                                                                                                                    Homo sapiens.
                   30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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determining polymorphic forms for use in e.g. forensics, paternity per determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease

Claim 1. Page 219; 310pp; English.

X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in contain the proposition of the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in methods for determining polymorphic forms in an individual for use in comparing polymorphic forms in a individual for use in methods for determining polymorphic forms in sapinguals. Lesch-Nyhan syndrome, could as agammaglobulinemia, diabetes inspituals, resch-Nyhan syndrome, muscular dystrophy, Wiskott-Aidrich syndrome, Rabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary controme, osteogenesis imperfecta, acute intermittent porphyria, syndrome, osteogenesis imperfecta, acute intermittent porphyria, syndrome diseases, inflammation, cancer, diseases of the nervous such actorimune diseases, inflammation, cancer, diseases of the nervous such as longevity, appearance (e.g. baldness, obestty), strength, speed, endurance, fertility, and susceptibility or receptivity to particular
                                                                                                                           Claim 1: Page 1720: 2245pp; Japanese.

Claim 1: Page 1720: 2245pp; Japanese.

Claim 1: Page 1720: 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

C double-stranded DNA) which comprises one of the 787 "Gs" sequences

Given in T19001-T26837 and which is able to hybridise to part of

C diman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

Sequences were obtained from 3'-directed cDNA libraries prepared

C from various human tissues; synthesis of cDNA was initiated from the

CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

CULTAINSTATE Sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

CS is constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC The appearance frequency of a given GS in a cDNA library can be

C determined (esp. using primers and probes derived from the GS

CC sequences) as a means of diagnosing abnormal cell function or for

C recognising different cell types.

SQ Sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
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Polymorphism: biallelic; human: forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid segments from the human genome - used for
reflects relative abundance of corresp. mRNA in specific human tissues
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06-NOV-1996; US-030455.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
HUGSON T, Lander ES, Wang D;
WPI; 98-286974/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9820165-A2.
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39 CAGGAGCTCAAGACCAKCCTGGGAAACATAGCAAGACTC 1

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as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                  30-MAR-1999 (first entry)
Human biallelic polymorphic DNA fragment EST98276c.
Folymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotyping; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
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Human gene signature HUMGS06998.

Gene signature; messenger RNA; mRNA; relative abundance; frequency;

Gene signature; messenger RNA; mRNA; relative abundance; frequency;

human; cloning; mapping; non-biased library; diagnosis; detection;

cell typing; abnormal cell function; ss.

HOMO sapiens

MO9514772-A1.

01-JUN-1995.

11-NOV-1994; J01916.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3698 CAGTAGTTCAAGACCAGCCTGGGCAACATGGAGAAACCC 3736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGAGCTCAAGACCATCCTGGGAAACATAGCAAGACTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63.4; DB Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.2%;
                                                                                                                      X12085 standard; DNA; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 76.8
nes 76; Conservative
                                                                                                                                                                                                                                                                                                               Homo saptens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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T24892/c
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                                                                                                                                                                                          1;
                                                                                                                                                                                                                                      16714 TGTATTTTAGTAGAGATAGGGTTTCACAATGCTGGCCAGGCTGGTCGTCAAACTCCTGCC 16773
drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1999 (first entry)

Human biallellc polymorphic DNA fragment EST98276a.

Polymorphism; biallellc; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid segments from the human genome - used for
                                                                                                                                                                                          1;
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                                                                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                16774 CTCAAGTGATCCTCCTGCCTCGGCCTCCC-AATGTGCTGGGATTACAG 16820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                      61 TICAAGTGATCCGTCTGCCTTGGCCTCCCAAAAGTGCTGGGATTATAG 108
                                                                                                                                                                                          17; Indels
                                                                           37 T;
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                                                                                                                                            Score 68.4; DB 1;
Pred. No. 0.16;
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Pred. No. 0.76;
1; Mismatches
                                                                                                                                                                                        1; Mismatches
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(WHED ) WHITEHEAD INST BIOMEDICAL RES.
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                                                                        23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prophylaxis of such diseases.
Sequence 100 BP; 21 A;
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                                                                                                                                            0.2%;
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                                                                           19 A;
                                                                                                                                     Ouery Match
Best Local Similarity 82.4%
Matches 89; Conservative
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Best Local Similarity 76.8
Matches 76; Conservative
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Length 100;

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WPI; 98-286974/25.

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                                                                                                                                                                                                A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences given in 719001-726837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end in the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular rissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 100 BP; 28 A; 22 C; 25 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16553 TTTTTTTTTTTTGAGATGGAGTCTTACTCTGTCGCTCAAGCTGCAGTGCAGTGCAAATC 16612
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Polymorphism, biallelic; human: forensic; paternity testing; disease;
detection; phenotypic typing; characteristic; infection; hereditary;
autoimmune disease; cancer; inflammation; drug; therapy; medicament,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 TITGITICATACAACAGAGIGACACTCTCTCACCCCAGGCNGGAGTGCAANGGIGCAATC 41
                                                                                                              reflects relative abundance of corresp. mRNA in specific human tissues
                                                                                 WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%; Score 62.4; DB 1; Length 100; 75.8%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 24; Indels
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X12086 standard; DNA; 100 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Conservative
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05-NOV-1997; U20313.
06-NOV-1996; US-030455.
12-NOV-1993; JP-355504
                                                                 Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment; marker; ss
                     (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9820165-A2.
                                                                     Matsubara K
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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNAs in almost is constructed so as to reflect accurately the relative abundance of different mRNAs. In the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 91 BP; 18 A; 22 C; 28 G; 18 T;
haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3638 GTGGCTCAAGCCTGTAATCCCAACACTTTGGGAGGCTAAGGTGGGAGGATTGCTTGAGCC 3697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GTGACTCACACCTATAATCCTGGCACTTTAGGAGGCTKAGGAAGGAGGAGTGTTTGAAAC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene signature HUMGS08084.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsubára K, Okubo K;
WPI; 95-206931/27.
Tdentlítying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
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                                                                                                                                                                                                                                                                                                               31 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                               22 G;
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                            25 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T25854 standard; cDNA to mRNA; 91
T25854;
                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%;
                                                                                                                                                                                                                                                                            prophylaxis of such diseases. Sequence 100 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.2%;
Best Local Similarity 78.7%;
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 76.8°
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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Claim 1; Page 2182; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 [63] sequences (given in T19001-T25687] and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNAs in amost is constructed so as to reflect accurately the relative abundance of different mRNAs. In the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS. sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28509 GATCTCTTGACCTTGTGATCCACCCGCCTCAGCCTCCCAAAGTGCCAGGATTACAGGCAT 28568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 2029; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 1from various human poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GATCTCCTGACCTCGTCATCCGCCCGTNTCGGCCTCCCATAGTGCTGGGNTTACAGGCAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.NOV-1996 (first entry)
Human gene signature HUMGSO8452.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
HOMO sapiens.
                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%; Score 61; DB 1; Length 108; 73.8%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy 28569 GAGCCACCGTGCCCAGCTTTTTTTTTTTTATAAGACAAG 28611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GAGCCACCACCACCGCCGCTGTTTATTCTTATAACTGTACAGG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recognising different cell types. Sequence 108 BP; 18 A; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 73.8°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
12-NOV-1993; JP-355504
                                                                             Okubo K;
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                        (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
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                                                                             Matsubara K, Okul
WPI; 95-206931/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences double-stranded DNA) which comprises one of the 7837 "GS" sequences of your in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-entiented sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 103 BP; 22 A; 27 C; 21 G; 31 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy 13607 CATGGCAAAACCCTGGCTCTACCAAAAATACAACAATTAGCTGGGCATTGTGGCACATGC 13666
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human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                       24-JUL-1996 (first entry)
Human gene signature HUMGSO2180.
Human gene signature: messenger RNA: mRNA: relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13667 CTGTAATCCCAGCTACTTGGGAGGCTGAAGCACAAGAATC 13706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13764 CCTGGGTGACAGAGAGATTCTGTCTCA 13792
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                                                    62 CCTNGGTGACAGCGTGAGANNCTGTCTCA 90
                                                                                                                                                                                7/c
T20927 standard; cDNA to mRNA; 103 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.28
Best Local Similarity 75.08
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB.) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okubo K;
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11-NOV-1994; J01916.
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WO9514772-A1.
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WO9514772-A1.
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Claim 1;
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Gaps

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27; Indels

1.6;

28 T;

23 G;

33 C;

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double-stranded DNA, which comprises one of the 7837 "GS" sequences
given in Tigodi-T26837 and which is able to hybridise to part of
the mind of the mind of the mind of the mind of the mind genomic DNA, cDNA or mixh is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed as as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
cetermined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
Sequence 108 BP; 18 A; 33 C; 23 G; 28 T;
                                                                                                                                                                                                                                                                                                                                                                              17856 GATTGCTTAAGCCCAGGAATTTAAGGCTGCAGGGAGCCATGATGGGGGCCATTGCACTCCA 17915
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                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-1996 (first entry)

Human gene signature HUMGS09078.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that
                        different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 103 BP; 33 A; 21 C; 25 G; 23 T;
constructed so as to reflect accurately the relative abundance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                               DB 1; Length 103;
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75.8%; Pred. No. 1.8;
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Best Local Similarity 76.0°
Matches 73; Conservative
                                                                                                                                                                                                                                                                                          Best Local Similarity 75.8
Matches 75; Conservative
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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WPI; 95-206931/27
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                                                                                                                                                                                                                                                                  Query Match
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or makA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed as as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 108 BP; 34 A; 31 C; 26 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17856 GATTGCTTAAGCCCCAGGAATTTAAGGCTGCAGGGAGCCATGATGGGGCCATTGCACTCCA 17915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                        Human gene signature HUMGS07131.
Gene signature; messenger RND, mRND, relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
W09514772-A1.
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Low frequency repeat; AluI restriction digest; genetic mapping; polymerase chain reaction; ss.
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76.6%; Pred. No. 2.6;
iive 0; Mismatches
36 GAGGCCGANACGGCCGGATGACGAGGTCAGGAGATC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCCTGAGTGACAGAGCCAGGTGTTGAAAACA 94
                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1748; 2245pp; Japanese.
                                                                                                                                          T25009 standard; cDNA to mRNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duncan CH, Kaplan DJ, Solus JF; WPI; 92-324992/40.
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                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS.) MATSUBARA K.
(OKUB/) OKUBO A...
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11-APR-1991; 105802.
28-MAR-1991; US-676292.
(UYWA-) UNIV WAYNE STATE.
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                                                                               RESULT
T25009
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PT New nucleic acid probes - have a labelled low frequency repetitive sequence for detecting overlaps among cloned DNA bas analysis.

PS Saciosure; Page 8; 41pp; English.

CC Genomic human placental DNA was mixed with a pair of PCR primers CC (see 029014 and 029015). The amplified DNA products were separated CC on an agarose gel and fragments were lighted DNA products were separated CC isolated. The fragments were lighted to Misnapl9 RF DNA from whic the 12bp SalI BamHI insert had been removed. Competent JM109 were con NZY plates contg. beta agalactosidase indicator dye. Duplicate CC filter replicates were screened with two probes, one taken from the con NZY plates contg. beta argalactosidase indicator dye. Duplicate CC internal region of an Alu repead (see 029016) and the other a 5kb fragment contg. an Li sequence from the region 5' to the human gamma globin gene. Phage plaques which did not hybridise to either CC probe and did not react with the dye indicator were selected. Single-stranded DNA was extracted from them to isolate low-frequency repeat sequence probes LF12, LF15, LF16, LF17, LF18 and LF22. CC Sequence 69 BP; 19 A; 18 C; 21 G; 11 T;
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Qy 13604 CAACATGG 13611

61 CAACATGG 68

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Search completed: June 16, 2000, 21:16:14 Job time: 202685 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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29001
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Listing first 45 summaries
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EWATYOLS: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

EL (bases I to 106)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashUr NCI human EST Project

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced g1:1397630.

Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA703692 106 bp mRNA EST 24-DEC-1997 ag81a10.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1140858 5' similar to contains Alu repetitive element;, mRNA
                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1127 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 102.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Email: est@watcon.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortlum (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                      109 CACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGTAGGGAGAT 50
        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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AQS7322 RPCI-11-4
AA250812 ZS06a05.s
AA583252 nn41e04.s
B65160 CIT-HSP-201
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AQ386882 RPCII1-13
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AA807640 nx08b05.s
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AA370029 EST81584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 109)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
  Description
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On Dec 3, 1996 this sequence version replaced gi:1126869.
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AQ386882
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Gaps

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30; Length 109; 7; Indels  $\sim$ 

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Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa; Catarrhini; Hominidae; Homo.

E Lobacia: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 110)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building

Unpublished (1997)

L Ontact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                            AQ386882 110 bp DNA GSS 21-MAY-1999
RPCI11-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
genomic survey sequence.
/note-"Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1; CalTech Human BAC Library D"

30 c 34 g 17 t
                                                                                                                                                                                        /cell_type="Lymphocytes"
//cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
26 c 38 g 20 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy 9524 GGGTTTCACCATGTTGGCCAGGCTGGTGTTGAACTCCTGACCTCAAGTGATCCACCTGCC 9583
                                                                                                                                                                                                           1 CCGGCGCAGAGTCTCACGCCTGTAATCCCAGCACTTTGGGAGACCAGGCGGGTGGATC 60
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Pred. No. 0.14;
0; Mismatches 12; Indels 0;
                                                                                                                  Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                Qy 24077 ACGAGGTCAGGAGATCAAGACCATCCTGGCCAACATGGTGAAACCC 24122
                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                   61 ACGAGGTCAGGAGATCAAGACCGTCCTGGCTAACATGGTGAAACCC 106
                                                                                                                DB 105;
                                                                                                              Score 91.6; DB
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:7551267"
/db_xref="taxon:9606"
/clone="RPCI-11-13414"
/clone_lib="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AQ386882.1 GI:4357905
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Best Local Similarity 89.19
Matches 98; Conservative
                                                                                                                                                     97; Conservative
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Best Local Similarity
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AQ386882/c
LOCUS
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SOURCE
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Unpublished (1998)
Cohter_GSSs: CITBI-E1-2509A2.TR
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ264176 106 bp DNA GSS 27-OCT-1998 CITBI-E1-2509A2.TF CITBI-E1 Homo sapiens genomic clone 2509A2, genomic survey sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2509A2"
 /clone_lib="CITBI-E1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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GSS.
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Best Local Similarity 92.4%;
Matches 97; Conservative
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ORGANISM
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ORIGIN
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AQ264176
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Gaps

ACCESSION

KEYWORDS

SOURCE

AQ282107

RESULT

a ò REFERENCE AUTHORS

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="INAGE:125473"
/clone_ib="Norl_CAPP_GG3"
/tissue_type="pooled germ cell tumors"
/tab.host="bl108"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                               Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                             Tumor Gene Index
Inpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151346.
Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 87.
Location/Qualifiers
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Pred. No.
  AA807640.
AA807640.1 GI:2877108
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TITLE
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AQ535244
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I (bases 1 to 105).

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Unpublished (1998).

Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11brary availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                      AQ282107 105 bp DNA GSS 27-APR-1999
RPCI11-94B21.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-94B21, 96082107
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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110 GGGTTTCACCATGTTGTCCAGGCTGGTCTTGAACTCCTGACCTCAAGCGATCCACCTGCC 51
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Pred. No. 0.34;
0; Mismatches 11; Indels 0;
                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="GDB:7535756"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11"
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9
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Best Local Similarity 89.5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 110)

NoT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tunnor Gene Index

On Jan 19, 1998 this sequence version replaced gi:2150764.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty_free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 834 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double-stranded cONA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28310 TGAGACGGAGTCTCACTCTGTCACCCCAGGCTGGAGTGCAGTGACGCTATCTCGGCTCACT 28369
                                                                 Email: est@atson.wustl.edu
Insert Size: 1316
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read
Insert Length: 1316 Std Brror: 0.00
Seq primer: MI3RPl
High quality sequence stop: 363.
Location/Qualifiers
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Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy 28370 GCACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGA 28418
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/organism="Homo sapiens"

/db_xref="GDB:419851"

/db_xref="taxon:9606"

/clone="IMAGE:47310"

/clone=lib="Soares infant brain INIB"
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AA897366.1 GI:3033986
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Local Similarity 86.2%;
les 94; Conservative
                      Tel: 314 286 1800
Fax: 314 286 1810
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               Zhao, S., Adams, W.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Nap Building
Map Building
Unpublished (1997)
Lotact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hobetighr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleterfede)ong med. buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@tessgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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M90506.rl Soares infant brain lNIB Homo sapiens cDNA clone
IMAGE:47310 5' similar to contains Alu repetitive element; contains
MER22 repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
27 c 27 g 18 t
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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On May 5, 1995 this sequence version replaced gi:798506.
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.3%; Score 85.4; DB 108; Length 103; 89.3%; Pred. No. 0.59; 11, Indels 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB.7621533"
/db_xref="taxon:9606"
/clone="RPCI-11-317H22"
/clone_lib="RPCI-11"
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The WashU-Merck EST Project
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H11143.1 GI:875963
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Matches 92; Conservative
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                                                                                                                                                                                                            Ander—"Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCL_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728811, and 729096-731399. Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryotta; Metazoa; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 110)

I (bases 1 to 110)

S Adams, M.D., Rounsley, S.D., Zhao, S., Fiteld, C.E., Bass, S., Linher, K., Goldan, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

L Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQUU3188 110 bp DNA GSS 14-APR-1999
RPCI11-1D10.TPN RPCI-11 Homo sapiens genomic clone RPCI-11-1D10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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86.2%; Pred. No. 0.64;
tive 0; Mismatches 15; Indels
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                                                                                                                                              /clone="IMAGE:1466067"
/clone_lib="Soares_NFL_T_GBC_S1"
primer: -40m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soares and M. Fatima Bonaldo.
27 c 29 g 32 t
                                                                                                /organism="Homo sapiens"
                      High quality sequence stop: 63.
Location/Qualifiers
                                                                                                                       /db_xref="taxon:9606
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                                                                                                                                                                                               /lab_host="DH10B"
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Unpublished (1997)
On Sep 12, 196 this sequence version replaced gi:1393355.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                      24037 CIGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGAATCACGAGGTCAGGAGATCAAGA 24096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nk42bll.sl NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1016157 3/
similar to contains Alu repetitive element;, mRNA sequence.
AAS65533
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 107)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                           /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 27 c 26 g. 35 t
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                           DB 94; Length 110;
0.64;
ches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 87.
Location/Qualifiers
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                                                                                                                                                                                                                                                                           Score 85; DB 9
Pred. No. 0.64;
0; Mismatches
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/db_xref="taxon:9606"
           /db_xref="taxon:9606"
/clone="RPCI-11-1D10"
/clone_lib="RPCI-11"
/sex="Male"
/db_xref-"GDB:7500081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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Best Local Similarity
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Gaps

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Indels

Length 109;

**Query Match** 

Matches

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BASE COUNT

DEFINITION

ACCESSION VERSION KEYWORDS

AA244173/c

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ORGANISM

SOURCE

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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/db_xref="texaon:9deptens"
/db_xref="texaon:9de0"
/clone="7H12D08"
/clone="7H12D08"
/clone="7H12D08"
/sex="female"
/sex="female"
/sex="female"
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National Human Genome Research Institute/NIH
49 Corvent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
TTE: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Touchman, J.W., Bulfard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D. 2006 expressed-sequence tags derived from human chromosome Genome con a libraries Genome Res. 7 (3), 281-292 (1997)
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                                                                                                                                         9478 CCCCTACCACCATGCCCGGCTAATTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGT 9537
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU7E003 105 bp mRNA EST 24-SEP-1999
7H12D08 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone
7H12D08, mRNA sequence.
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Apr 14, 1993 this sequence version replaced gi:693433. Contact: Eric D. Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 28; Length 105;
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         4; DB 30;
0.75;
                                                                                                                                                                                                                                                                                                   49 TGGCCAGGCTGTCATGAACTCCTGACCGTAGGTGATCCACC 8
                                                                            11;
                Score 84.4; DB:
Pred. No. 0.75;
0; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: egreen@nhgrl.nih.gov
Plate: 12 row: D column: 08
Seq primer: -21M13 (ABI).
Location/Qualifiers
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                   0.3%;
Query Match
Best Local Similarity 89.29
watches 91; Conservative
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Best Local Similarity 8b./.
Best Local Similarity 8b./.
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On No. 29, 1993 this sequence version replaced gi:430513.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

M.D., Michael Emmert-Buck, M.D. Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
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1 (bases 1 to 109)

NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

NCI-CGAP procer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                13657 TGGCACATGCCTGTAATCCCAGCTACTTGGGAGGCTGAAGCACAAGAATCACTTGAACCG 13716
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                AA244173 109 bp mRNA EST 20-AUG-1997 nc05h06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007291 similar to contains Alu repetitive element;, mRNA sequence. AA244173
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                                                                                                                                      Length 107;
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High quality sequence stop: 90.
Location/Qualifiers
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28 c 31 g 22 t
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/clone_lib="NCI_CGAP_Pr1"
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                                                                                                                                      Score 84.6;
Pred. No. 0.
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/db_xref="taxon:9606"
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                56
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                                                                                                                                   ch 0.3%;
1 Similarity 86.9%;
93; Conservative
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FEATURES

BASE COUNT ORIGIN

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                                                                   ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On Jan 24, 1995 this sequence version replaced g1:634306.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Pred. No. 1.1;
0; Mismatches 13;
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High quality sequence stop: 90.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1007406"
/clone_lib="NCI_CGAP_Prl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                       mRNA
                                                                                                                                                      AA244245
AA244245.1 GI:1875104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%;
ilarity 87.4%;
Conservative
                                                                                       110 bp
                                                                                                                                                                                                                                                Homo sapiens
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                                                                                       AA244245
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                                                                                                                                                                                                                             human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                            DEFINITION
                                                                                                                                                                                                                                                ORGANISM
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ORIGIN
                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                AA244245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                           SOURCE
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RESULT 1 AQ386882

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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@deJong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
AQ386882 110 bp DNA GSS 21-MAY-1999
RPCII1-13414.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13414,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lydao, S., Adams, M.D., Nlerman, W., Malek, J., de Jong, P. and Venter, J.C.
Venter
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCCGCGCACCACGCCTCTAATCCAAGTACTTTGCGAGGCTGAGGCAGGTGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY 13570 TCACTIGAAGCCAGGAGTTCAAGACCAGCCTGCCCAACATGGCAAAACCC 13619
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Pred. No. 1.1;
0; Mismatches 17; Indels
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/db_xref="GDB:7551267"
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/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 g
                                                                    genomic survey sequence. AQ386882
                                                                                                                                                                                                                             AQ386882.1 GI:4357905
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Best Local Similarity 84.5%;
Matches 93; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 c
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